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 influenza A 3'-sequence

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<210> 6
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<220>
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 influenza A 3'-sequence

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12

<210> 7
 <211> 13
 <212> RNA
 <213> Influenza A virus

<400> 7
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 <212> RNA
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<400> 9
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1007337-020800

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<210> 15
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1007337-62882

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influenza C 3'-sequence

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<212> DNA

<213> Influenza A virus

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<210> 21

<211> 32

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acaaagtgtc gcccgagta ctggtcgacc tccgaagttg ggggggagcg aaagcaggca 180

aaccatttga atg gat gtc aat ccg act tta ctg ttc ttg aaa gtt cct 229

Met Asp Val Asn Pro Thr Leu Leu Phe Leu Lys Val Pro
1 5 10

gcg caa aat gca ata agt act acg ttc cct tac act gga gat cct cca 277

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tac agc cat gga aca ggg aca gga tac acc atg gac aca gtc aac agg 325

Tyr Ser His Gly Thr Gly Thr Gly Tyr Thr Met Asp Thr Val Asn Arg
30 35 40 45

aca cat caa tat tcg gaa aag ggg aaa tgg aca aca aac act gag act 373

Thr His Gln Tyr Ser Glu Lys Gly Lys Trp Thr Thr Asn Thr Glu Thr
50 55 60

gga gca ccc caa ctt aat cca att gat ggc cca ttg cct gag gac aat 421

Gly Ala Pro Gln Leu Asn Pro Ile Asp Gly Pro Leu Pro Glu Asp Asn
65 70 75

1007337-020802

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Phe	Leu	Glu	Glu	Ser	His	Pro	Gly	Ile	Phe	Glu	Asn	Ser	Cys	Leu	Glu	
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Thr	Met	Glu	Val	Val	Gln	Gln	Thr	Arg	Val	Asp	Lys	Leu	Thr	Gln	Gly	
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Arg	Gln	Thr	Tyr	Asp	Trp	Thr	Leu	Asn	Arg	Asn	Gln	Pro	Ala	Ala	Thr	
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gca	tta	gca	aac	act	ata	gag	gtc	ttt	aga	tcg	aat	ggg	cta	aca	gct	661
Ala	Leu	Ala	Asn	Thr	Ile	Glu	Val	Phe	Arg	Ser	Asn	Gly	Leu	Thr	Ala	
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Asn	Glu	Ser	Gly	Arg	Leu	Ile	Asp	Phe	Leu	Lys	Asp	Val	Met	Glu	Ser	
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Met	Asp	Lys	Glu	Glu	Met	Glu	Ile	Thr	Thr	His	Phe	Gln	Arg	Lys	Arg	
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Leu	Thr	Leu	Asn	Thr	Met	Thr	Lys	Asp	Ala	Glu	Arg	Gly	Lys	Leu	Lys	
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Phe	Val	Glu	Thr	Leu	Ala	Arg	Ser	Ile	Cys	Glu	Lys	Leu	Glu	Gln	Ser	
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agg cta ggg aaa ggg tac atg ttc gaa agc aaa agc atg aag ctc cga 1285
 Arg Leu Gly Lys Gly Tyr Met Phe Glu Ser Lys Ser Met Lys Leu Arg
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aca caa ata cca gca gaa atg cta gca agt att gat cta aaa tat ttc 1333
 Thr Gln Ile Pro Ala Glu Met Leu Ala Ser Ile Asp Leu Lys Tyr Phe
 370 375 380

aat gaa cca aca agg aag aaa atc gag aaa ata agg cct ctc ata ata 1381
 Asn Glu Pro Thr Arg Lys Lys Ile Glu Lys Ile Arg Pro Leu Ile Ile
 385 390 395

gac ggc aca gcc tca tta agc ccg gga atg atg atg ggt atg ttc aac 1429
 Asp Gly Thr Ala Ser Leu Ser Pro Gly Met Met Met Gly Met Phe Asn
 400 405 410

atg ctg agt aca gtg ttg gga gtc tca atc ctg aat ctt ggg caa aag 1477
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 415 420 425

aga tac acc aaa acc aca tac tgg tgg gat gga ctt cag tcc tct gat 1525
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 430 435 440 445

gat ttt gct ctc atc gtg aat gca cca aat cat gag gga ata caa gcg 1573
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 465 470 475

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 Ser Lys Lys Lys Ser Tyr Ile Asn Arg Thr Gly Thr Phe Glu Phe Thr
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gca aca gcc caa atg gct ctc caa tta ttc atc aag gac tac aga tat 1861
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 545 550 555

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 Thr Tyr Arg Cys His Arg Gly Asp Thr Gln Ile Gln Thr Arg Arg Ser
 560 565 570

ttc gag cta aag aag ctg tgg gag cag acc cgc tca aag gca gga ctg 1957
 Phe Glu Leu Lys Lys Leu Trp Glu Gln Thr Arg Ser Lys Ala Gly Leu
 575 580 585

ttg gtt tca gat ggc gga cca aac ctg tac aac att cgg aat ctc cac 2005
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 Gly Arg Leu Cys Asn Pro Met Asn Pro Phe Val Ser His Lys Glu Ile
 625 630 635

gaa tct gta aac aat gct gcg gta atg cca gcc cat ggt cca gcc aaa 2149
 Glu Ser Val Asn Asn Ala Ala Val Met Pro Ala His Gly Pro Ala Lys
 640 645 650

agc atg gaa tat gat gct gtg gca act aca cac tct tgg atc cct aag 2197
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 655 660 665

aga aac cgt tcc att ctg aat acg agt caa agg gga atc ctt gag gat 2245
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gaa caa atg tac cag aag tgt tgc aac cta ttc gag aaa ttc ttc cct 2293
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<210> 23

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<223> Description of Artificial Sequence: FPV-Br.-PB1

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Gly Thr Gly Thr Gly Tyr Thr Met Asp Thr Val Asn Arg Thr His Gln
35 40 45

Tyr Ser Glu Lys Gly Lys Trp Thr Thr Asn Thr Glu Thr Gly Ala Pro
50 55 60

Gln Leu Asn Pro Ile Asp Gly Pro Leu Pro Glu Asp Asn Glu Pro Ser
65 70 75 80

Gly Tyr Ala Gln Thr Asp Cys Val Leu Glu Ala Met Ala Phe Leu Glu
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Glu Ser His Pro Gly Ile Phe Glu Asn Ser Cys Leu Glu Thr Met Glu
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115 120 125

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130 135 140

Asn Thr Ile Glu Val Phe Arg Ser Asn Gly Leu Thr Ala Asn Glu Ser
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Gly Arg Leu Ile Asp Phe Leu Lys Asp Val Met Glu Ser Met Asp Lys
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Glu Glu Met Glu Ile Thr Thr His Phe Gln Arg Lys Arg Arg Val Arg
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Asp Asn Met Thr Lys Lys Met Val Thr Gln Arg Thr Ile Gly Lys Lys
195 200 205

Lys Gln Arg Leu Asn Lys Arg Ser Tyr Leu Ile Arg Ala Leu Thr Leu
210 215 220

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Ile Ala Thr Pro Gly Met Gln Ile Arg Gly Phe Val Tyr Phe Val Glu
245 250 255

Thr Leu Ala Arg Ser Ile Cys Glu Lys Leu Glu Gln Ser Gly Leu Pro
260 265 270

Val Gly Gly Asn Glu Lys Lys Ala Lys Leu Ala Asn Val Val Arg Lys
275 280 285

Met Met Thr Asn Ser Gln Asp Thr Glu Leu Ser Phe Thr Ile Thr Gly
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Asp Asn Thr Lys Trp Asn Glu Asn Gln Asn Pro Arg Met Phe Leu Ala
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Met Ile Thr Tyr Ile Thr Arg Asn Gln Pro Glu Trp Phe Arg Asn Val
325 330 335

Leu Ser Ile Ala Pro Ile Met Phe Ser Asn Lys Met Ala Arg Leu Gly
 340 345 350
 Lys Gly Tyr Met Phe Glu Ser Lys Ser Met Lys Leu Arg Thr Gln Ile
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 Ala Ser Leu Ser Pro Gly Met Met Met Gly Met Phe Asn Met Leu Ser
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 Cys His Arg Gly Asp Thr Gln Ile Gln Thr Arg Arg Ser Phe Glu Leu
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 Asn Asn Ala Ala Val Met Pro Ala His Gly Pro Ala Lys Ser Met Glu
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10073377-000000

Leu Arg Arg Gln. Lys
755

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Thr Met Glu Val Val Gln Gln Thr Arg Val Asp Lys Leu Thr Gln Gly
110 115 120 125

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 Asn Glu Ser Gly Arg Leu Ile Asp Phe Leu Lys Asp Val Met Glu Ser
 160 165 170

atg aac aaa gaa gaa atg gag atc aca act cat ttt cag aga aag aga 757
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cga gtg aga gac aat atg act aag aaa atg gtg aca cag aga aca ata 805
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 190 195 200 205

ggt aaa agg aag cag aga ttg aac aaa agg agt tat cta att agg gca 853
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 210 215 220

tta acc ctg aac aca atg acc aaa gat gct gag aga ggg aag cta aaa 901
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 225 230 235

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 240 245 250

ttt gtt gag aca cta gca agg agt ata tgt gag aaa ctt gaa caa tca 997
 Phe Val Glu Thr Leu Ala Arg Ser Ile Cys Glu Lys Leu Glu Gln Ser
 255 260 265

gga ttg cca gtt gga ggc aat gag aag aaa gca aag ttg gca aat gtt 1045
 Gly Leu Pro Val Gly Gly Asn Glu Lys Lys Ala Lys Leu Ala Asn Val
 270 275 280 285

gta agg aag atg atg acc aat tct cag gac act gaa att tct ttc acc 1093
 Val Arg Lys Met Met Thr Asn Ser Gln Asp Thr Glu Ile Ser Phe Thr
 290 295 300

atc act gga gat aac acc aaa tgg aac gaa aat cag aac cct cgg atg 1141
 Ile Thr Gly Asp Asn Thr Lys Trp Asn Glu Asn Gln Asn Pro Arg Met
 305 310 315

ttt ttg gcc atg atc aca tat ata acc aga aat cag ccc gaa tgg ttc 1189
 Phe Leu Ala Met Ile Thr Tyr Ile Thr Arg Asn Gln Pro Glu Trp Phe
 320 325 330

aga aat gtt cta agt att gct cca ata atg ttc tca aac aaa atg gcg 1237
 Arg Asn Val Leu Ser Ile Ala Pro Ile Met Phe Ser Asn Lys Met Ala
 335 340 345

aga ctg gga aag ggg tac atg ttt gag agc aag agt atg aaa att aga 1285
 Arg Leu Gly Lys Gly Tyr Met Phe Glu Ser Lys Ser Met Lys Ile Arg
 350 355 360 365

act caa ata cct gca gaa atg cta gca agc atc gat ttg aaa tac ttc 1333
 Thr Gln Ile Pro Ala Glu Met Leu Ala Ser Ile Asp Leu Lys Tyr Phe
 370 375 380

aat gat tca act aga aag aag att gaa aaa atc cgg ccg ctc tta ata 1381
 Asn Asp Ser Thr Arg Lys Lys Ile Glu Lys Ile Arg Pro Leu Leu Ile
 385 390 395

10073377-020806

gat Asp	ggg Gly	act Thr	gca Ala	tca Ser	ttg Leu	agc Ser	cct Pro	gga Gly	atg Met	atg Met	atg Met	ggc Gly	atg Met	ttc Phe	aat Asn	1429
		400					405					410				
atg Met	tta Leu	agt Ser	act Thr	gta Val	tta Leu	ggc Gly	gtc Val	tcc Ser	atc Ile	ctg Leu	aat Asn	ctt Leu	gga Gly	caa Gln	aag Lys	1477
	415					420					425					
aga Arg	cac His	acc Thr	aag Lys	act Thr	act Thr	tac Tyr	tgg Trp	tgg Trp	gat Asp	ggt Gly	ctt Leu	caa Gln	tct Ser	tct Ser	gat Asp	1525
430					435					440					445	
gat Asp	ttt Phe	gct Ala	ctg Leu	att Ile	gtg Val	aat Asn	gca Ala	ccc Pro	aat Asn	cat His	gaa Glu	ggg Gly	att Ile	caa Gln	gcc Ala	1573
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			465					470					475			
agc Ser	aag Lys	aaa Lys	aag Lys	tct Ser	tac Tyr	ata Ile	aac Asn	aga Arg	aca Thr	ggt Gly	aca Thr	ttt Phe	gaa Glu	ttc Phe	aca Thr	1669
		480					485					490				
agc Ser	ttt Phe	ttc Phe	tat Tyr	cgt Arg	tat Tyr	ggg Gly	ttt Phe	gtt Val	gcc Ala	aat Asn	ttc Phe	agc Ser	atg Met	gag Glu	ctt Leu	1717
	495					500					505					
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	575					580					585					
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590				595					600						605	
att Ile	cct Pro	gaa Glu	gtc Val	tgc Cys	ttg Leu	aaa Lys	tgg Trp	gaa Glu	tta Leu	atg Met	gat Asp	gag Glu	gat Asp	tac Tyr	cag Gln	2053
				610					615					620		
ggg Gly	cgt Arg	tta Leu	tgc Cys	aac Asn	cca Pro	ctg Leu	aac Asn	cca Pro	ttt Phe	gtc Val	aac Asn	cat His	aaa Lys	gac Asp	att Ile	2101
			625					630					635			
gaa Glu	tca Ser	gtg Val	aac Asn	aat Asn	gca Ala	gtg Val	ata Ile	atg Met	cca Pro	gca Ala	cat His	ggt Gly	cca 			

tctgacgctc agtggaaacga aaactcacgt taagggattt tgggtcatgag tattatcaaaa 369:

aggatcttca cctagatcct tttaaattaa aaatgaagtt tttaatcaat cttaaagtata 3751
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 ttgcttcgca acgttcaaat ccgctcccg cggatttgct ctactcagga gagcgttcac 4891
 cgacaaacaa cagataaaac gaaaggccca gtctttcgac tgagcctttc gttttatttg 4951
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<211> 757

<212> PRT

<213> Artificial Sequence

<223> Description of Artificial Sequence: WSN-PB1

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Gly Thr Gly Thr Gly Tyr Thr Met Asp Thr Val Asn Arg Thr His Gln
 35 40 45

Tyr	Ser	Glu	Arg	Gly	Arg	Trp	Thr	Thr	Asn	Thr	Glu	Thr	Gly	Ala	Pro
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Gln	Leu	Asn	Pro	Ile	Asp	Gly	Pro	Leu	Pro	Glu	Asp	Asn	Glu	Pro	Ser
65					70					75					80
Gly	Tyr	Ala	Gln	Thr	Asp	Cys	Val	Leu	Glu	Ala	Met	Ala	Phe	Leu	Glu
				85					90					95	
Glu	Ser	His	Pro	Gly	Ile	Phe	Glu	Thr	Ser	Cys	Leu	Glu	Thr	Met	Glu
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Val	Val	Gln	Gln	Thr	Arg	Val	Asp	Lys	Leu	Thr	Gln	Gly	Arg	Gln	Thr
		115					120					125			
Tyr	Asp	Trp	Thr	Leu	Asn	Arg	Asn	Gln	Pro	Ala	Ala	Thr	Ala	Leu	Ala
	130					135					140				
Asn	Thr	Ile	Glu	Val	Phe	Arg	Ser	Asn	Gly	Leu	Thr	Ala	Asn	Glu	Ser
145					150					155					160
Gly	Arg	Leu	Ile	Asp	Phe	Leu	Lys	Asp	Val	Met	Glu	Ser	Met	Asn	Lys
				165					170					175	
Glu	Glu	Met	Glu	Ile	Thr	Thr	His	Phe	Gln	Arg	Lys	Arg	Arg	Val	Arg
			180					185					190		
Asp	Asn	Met	Thr	Lys	Lys	Met	Val	Thr	Gln	Arg	Thr	Ile	Gly	Lys	Arg
		195					200					205			
Lys	Gln	Arg	Leu	Asn	Lys	Arg	Ser	Tyr	Leu	Ile	Arg	Ala	Leu	Thr	Leu
	210					215					220				
Asn	Thr	Met	Thr	Lys	Asp	Ala	Glu	Arg	Gly	Lys	Leu	Lys	Arg	Arg	Ala
225					230					235					240
Ile	Ala	Thr	Pro	Gly	Met	Gln	Ile	Arg	Gly	Phe	Val	Tyr	Phe	Val	Glu
				245					250					255	
Thr	Leu	Ala	Arg	Ser	Ile	Cys	Glu	Lys	Leu	Glu	Gln	Ser	Gly	Leu	Pro
			260					265					270		
Val	Gly	Gly	Asn	Glu	Lys	Lys	Ala	Lys	Leu	Ala	Asn	Val	Val	Arg	Lys
		275					280					285			
Met	Met	Thr	Asn	Ser	Gln	Asp	Thr	Glu	Ile	Ser	Phe	Thr	Ile	Thr	Gly
	290					295					300				
Asp	Asn	Thr	Lys	Trp	Asn	Glu	Asn	Gln	Asn	Pro	Arg	Met	Phe	Leu	Ala
305					310					315					320
Met	Ile	Thr	Tyr	Ile	Thr	Arg	Asn	Gln	Pro	Glu	Trp	Phe	Arg	Asn	Val
				325					330					335	
Leu	Ser	Ile	Ala	Pro	Ile	Met	Phe	Ser	Asn	Lys	Met	Ala	Arg	Leu	Gly
			340					345					350		
Lys	Gly	Tyr	Met	Phe	Glu	Ser	Lys	Ser	Met	Lys	Ile	Arg	Thr	Gln	Ile
		355					360					365			
Pro	Ala	Glu	Met	Leu	Ala	Ser	Ile	Asp	Leu	Lys	Tyr	Phe	Asn	Asp	Ser
	370					375					380				
Thr	Arg	Lys	Lys	Ile	Glu	Lys	Ile								

Ala Ser Leu Ser Pro Gly Met Met Met Gly Met Phe Asn Met Leu Ser
 405 410 415
 Thr Val Leu Gly Val Ser Ile Leu Asn Leu Gly Gln Lys Arg His Thr
 420 425 430
 Lys Thr Thr Tyr Trp Trp Asp Gly Leu Gln Ser Ser Asp Asp Phe Ala
 435 440 445
 Leu Ile Val Asn Ala Pro Asn His Glu Gly Ile Gln Ala Gly Val Asn
 450 455 460
 Arg Phe Tyr Arg Thr Cys Lys Leu Leu Gly Ile Asn Met Ser Lys Lys
 465 470 475 480
 Lys Ser Tyr Ile Asn Arg Thr Gly Thr Phe Glu Phe Thr Ser Phe Phe
 485 490 495
 Tyr Arg Tyr Gly Phe Val Ala Asn Phe Ser Met Glu Leu Pro Ser Phe
 500 505 510
 Gly Val Ser Gly Ile Asn Glu Ser Ala Asp Met Ser Ile Gly Val Thr
 515 520 525
 Val Ile Lys Asn Asn Met Ile Asn Asn Asp Leu Gly Pro Ala Thr Ala
 530 535 540
 Gln Met Ala Leu Gln Leu Phe Ile Lys Asp Tyr Arg Tyr Thr Tyr Arg
 545 550 555 560
 Cys His Arg Gly Asp Thr Gln Ile Gln Thr Arg Arg Ser Phe Glu Ile
 565 570 575
 Lys Lys Leu Trp Glu Gln Thr His Ser Lys Ala Gly Leu Leu Val Ser
 580 585 590
 Asp Gly Gly Pro Asn Leu Tyr Asn Ile Arg Asn Leu His Ile Pro Glu
 595 600 605
 Val Cys Leu Lys Trp Glu Leu Met Asp Glu Asp Tyr Gln Gly Arg Leu
 610 615 620
 Cys Asn Pro Leu Asn Pro Phe Val Asn His Lys Asp Ile Glu Ser Val
 625 630 635 640
 Asn Asn Ala Val Ile Met Pro Ala His Gly Pro Ala Lys Asn Met Glu
 645 650 655
 Tyr Asp Ala Val Ala Thr Thr His Ser Trp Ile Pro Lys Arg Asn Arg
 660 665 670
 Ser Ile Leu Asn Thr Ser Gln Arg Gly Ile Leu Glu Asp Glu Gln Met
 675 680 685
 Tyr Gln Lys Cys Cys Asn Leu Phe Glu Lys Phe Phe Pro Ser Ser Ser
 690 695 700
 Tyr Arg Arg Pro Val Gly Ile Ser Ser Met Val Glu Ala Met Val Ser
 705 710 715 720
 Arg Ala Arg Ile Asp Ala Arg Ile Asp Phe Glu Ser Gly Arg Ile Lys
 725 730 735
 Lys Glu Glu Phe Thr Glu Ile Met Lys Ile Cys Ser Thr Ile Glu Glu
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1007377-020002

Leu Arg Arg Gln Lys
755

<210> 26
<211> 5169
<212> DNA
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<220>
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acaaagtgtc gcccggagta ctggtcgacc tccgaagttg ggggggagcg aaagcaggca 180
aaccatttga atg gat gtc aat ccg act tta ctt ttc tta aaa gtg cca 229
Met Asp Val Asn Pro Thr Leu Leu Phe Leu Lys Val Pro
1 5 10
gca caa aat gct ata agc aca act ttc cct tat act gga gac cct cct 277
Ala Gln Asn Ala Ile Ser Thr Thr Phe Pro Tyr Thr Gly Asp Pro Pro
15 20 25
tac agc cat ggg aca gga aca gga tac acc atg gat act gtc aac agg 325
Tyr Ser His Gly Thr Gly Thr Gly Tyr Thr Met Asp Thr Val Asn Arg
30 35 40 45
aca cat cag tac tca gaa agg gga aga tgg aca aca aac acc gaa act 373
Thr His Gln Tyr Ser Glu Arg Gly Arg Trp Thr Thr Asn Thr Glu Thr
50 55 60
gga gca ccg caa ctc aac ccg att gat ggg cca ctg cca gaa gac aat 421
Gly Ala Pro Gln Leu Asn Pro Ile Asp Gly Pro Leu Pro Glu Asp Asn
65 70 75
gaa cca agt ggt tat gcc caa aca gat tgt gta ttg gaa gca atg gcc 469
Glu Pro Ser Gly Tyr Ala Gln Thr Asp Cys Val Leu Glu Ala Met Ala
80 85 90
ttc ctt gag gaa tcc cat cct ggt atc ttt gag acc tcg tgt ctt gaa 517
Phe Leu Glu Glu Ser His Pro Gly Ile Phe Glu Thr Ser Cys Leu Glu
95 100 105
acg atg gag gtt gtt cag caa aca cga gtg gac aag ctg aca caa ggc 565
Thr Met Glu Val Val Gln Gln Thr Arg Val Asp Lys Leu Thr Gln Gly
110 115 120 125
cga cag acc tat gac tgg act cta aat agg aac cag cct gct gca aca 613
Arg Gln Thr Tyr Asp Trp Thr Leu Asn Arg Asn Gln Pro Ala Ala Thr
130 135 140
gca ttg gcc aac aca ata gaa gtg ttc aga tca aat ggc ctc acg gcc 661
Ala Leu Ala Asn Thr Ile Glu Val Phe Arg Ser Asn Gly Leu Thr Ala
145 150 155
aat gaa tct gga agg ctc ata gac ttc ctt aag gat gta atg gag tca 709
Asn Glu Ser Gly Arg Leu Ile Asp Phe Leu Lys Asp Val Met Glu Ser
160 165 170

1007337-000000

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Met	Asn	Lys	Glu	Glu	Met	Glu	Ile	Thr	Thr	His	Phe	Gln	Arg	Lys	Arg	
175						180					185					
cga	gtg	aga	gac	aat	atg	act	aag	aaa	atg	gtg	aca	cag	aga	aca	ata	805
Arg	Val	Arg	Asp	Asn	Met	Thr	Lys	Lys	Met	Val	Thr	Gln	Arg	Thr	Ile	
190					195					200					205	
ggt	aaa	agg	aag	cag	aga	ttg	aac	aaa	agg	agt	tat	cta	att	agg	gca	853
Gly	Lys	Arg	Lys	Gln	Arg	Leu	Asn	Lys	Arg	Ser	Tyr	Leu	Ile	Arg	Ala	
				210					215					220		
tta	acc	ctg	aac	aca	atg	acc	aaa	gat	gct	gag	aga	ggg	aag	cta	aaa	901
Leu	Thr	Leu	Asn	Thr	Met	Thr	Lys	Asp	Ala	Glu	Arg	Gly	Lys	Leu	Lys	
			225					230					235			
cgg	aga	gca	att	gca	acc	cca	ggg	atg	caa	ata	agg	ggg	ttt	gta	tac	949
Arg	Arg	Ala	Ile	Ala	Thr	Pro	Gly	Met	Gln	Ile	Arg	Gly	Phe	Val	Tyr	
		240					245					250				
ttt	gtt	gag	aca	cta	gca	agg	agt	ata	tgt	gag	aaa	ctt	gaa	caa	tca	997
Phe	Val	Glu	Thr	Leu	Ala	Arg	Ser	Ile	Cys	Glu	Lys	Leu	Glu	Gln	Ser	
	255					260					265					
gga	ttg	cca	gtt	gga	ggc	aat	gag	aag	aaa	gca	aag	ttg	gca	aat	gtt	1045
Gly	Leu	Pro	Val	Gly	Gly	Asn	Glu	Lys	Lys	Ala	Lys	Leu	Ala	Asn	Val	
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gta	agg	aag	atg	atg	acc	aat	tct	cag	gac	act	gaa	att	tct	ttc	acc	1093
Val	Arg	Lys	Met	Met	Thr	Asn	Ser	Gln	Asp	Thr	Glu	Ile	Ser	Phe	Thr	
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atc	act	gga	gat	aac	acc	aaa	tgg	aac	gaa	aat	cag	aac	cct	cgg	atg	1141
Ile	Thr	Gly	Asp	Asn	Thr	Lys	Trp	Asn	Glu	Asn	Gln	Asn	Pro	Arg	Met	
			305					310					315			
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Phe	Leu	Ala	Met	Ile	Thr	Tyr	Ile	Thr	Arg	Asn	Gln	Pro	Glu	Trp	Phe	
		320					325					330				
aga	aat	gtt	cta	agt	att	gct	cca	ata	atg	ttc	tca	aac	aaa	atg	gcg	1237
Arg	Asn	Val	Leu	Ser	Ile	Ala	Pro	Ile	Met	Phe	Ser	Asn	Lys	Met	Ala	
	335					340					345					
aga	ctg	gga	aag	ggg	tac	atg	ttt	gag	agc	aag	agt	atg	aaa	att	aga	1285
Arg	Leu	Gly	Lys	Gly	Tyr	Met	Phe	Glu	Ser	Lys	Ser	Met	Lys	Ile	Arg	
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act	caa	ata	cct	gca	gaa	atg	cta	gca	agc	atc	gat	ttg	aaa	tac	ttc	1333
Thr	Gln	Ile	Pro	Ala	Glu	Met	Leu	Ala	Ser	Ile	Asp	Leu	Lys	Tyr	Phe	
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aat	gat</															

gat	ttt	gct	ctg	att	gtg	aat	gca	ccc	aat	cat	gaa	ggg	att	caa	gcc	1573
Asp	Phe	Ala	Leu	Ile	Val	Asn	Ala	Pro	Asn	His	Glu	Gly	Ile	Gln	Ala	
			450						455					460		
gga	gtc	aac	agg	ttt	tat	cga	acc	tgt	aag	cta	ctt	gga	att	aat	atg	1621
Gly	Val	Asn	Arg	Phe	Tyr	Arg	Thr	Cys	Lys	Leu	Leu	Gly	Ile	Asn	Met	
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agc	aag	aaa	aag	tct	tac	ata	aac	aga	aca	ggg	aca	ttt	gaa	ttc	aca	1669
Ser	Lys	Lys	Lys	Ser	Tyr	Ile	Asn	Arg	Thr	Gly	Thr	Phe	Glu	Phe	Thr	
		480					485					490				
agc	ttt	ttc	tac	cgc	tat	gga	ttt	gta	gcc	aat	ttt	agt	atg	gag	ttg	1717
Ser	Phe	Phe	Tyr	Arg	Tyr	Gly	Phe	Val	Ala	Asn	Phe	Ser	Met	Glu	Leu	
	495					500					505					
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Pro	Ser	Phe	Gly	Val	Ser	Gly	Ile	Asn	Glu	Ser	Ala	Asp	Met	Ser	Ile	
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Gly	Val	Thr	Val	Ile	Lys	Asn	Asn	Met	Ile	Asn	Asn	Asp	Leu	Gly	Pro	
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gca	aca	gcc	caa	atg	gct	ctc	caa	tta	ttc	atc	aag	gac	tac	aga	tat	1861
Ala	Thr	Ala	Gln	Met	Ala	Leu	Gln	Leu	Phe	Ile	Lys	Asp	Tyr	Arg	Tyr	
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Phe	Glu	Leu	Lys	Lys	Leu	Trp	Glu	Gln	Thr	Arg	Ser	Lys	Ala	Gly	Leu	
	575					580					585					
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Leu	Val	Ser	Asp	Gly	Gly	Pro	Asn	Leu	Tyr	Asn	Ile	Arg	Asn	Leu	His	
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atc	ccg	gaa	gtt	tgc	ctg	aaa	tgg	gaa	cta	atg	gat	gaa	gac	tat	cag	2053
Ile	Pro	Glu	Val	Cys	Leu	Lys	Trp	Glu	Leu	Met	Asp	Glu	Asp	Tyr	Gln	
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gga	aga	ctt	tgt	aat	ccc	atg	aac	ccg	ttt	gtc	agt	cat	aag	gaa	att	2101
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gaa	tct	gta	aac	aat	gct	gcg	gta	atg	cca	gcc	cat	ggg	cca	gcc	aaa	2149
Glu	Ser	Val	Asn	Asn	Ala	Ala	Val	Met	Pro	Ala	His	Gly	Pro	Ala	Lys	
			640				645					650				
agc	atg															

agc agc tca tac aga aga cca gtt gga att tcc agt atg gtg gag gcc	2341
Ser Ser Ser Tyr Arg Arg Pro Val Gly Ile Ser Ser Met Val Glu Ala	
705 710 715	
atg gtg tct agg gcc cgg att gat gca cga att gac ttc gag tct gga	2389
Met Val Ser Arg Ala Arg Ile Asp Ala Arg Ile Asp Phe Glu Ser Gly	
720 725 730	
agg att aag aag gaa gag ttt gct gag atc atg aag atc tgt tcc acc	2437
Arg Ile Lys Lys Glu Glu Phe Ala Glu Ile Met Lys Ile Cys Ser Thr	
735 740 745	
att gaa gag ctg aga cgg caa aaa tagtgaattt agcttgtcct tcatgaaaaa	2491
Ile Glu Glu Leu Arg Arg Gln Lys	
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 <223> Description of Artificial Sequence: pHL3102

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 Gly Thr Gly Thr Gly Tyr Thr Met Asp Thr Val Asn Arg Thr His Gln
 35 40 45
 Tyr Ser Glu Arg Gly Arg Trp Thr Thr Asn Thr Glu Thr Gly Ala Pro
 50 55 60
 Gln Leu Asn Pro Ile Asp Gly Pro Leu Pro Glu Asp Asn Glu Pro Ser
 65 70 75 80
 Gly Tyr Ala Gln Thr Asp Cys Val Leu Glu Ala Met Ala Phe Leu Glu
 85 90 95
 Glu Ser His Pro Gly Ile Phe Glu Thr Ser Cys Leu Glu Thr Met Glu
 100 105 110

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Val Val Gln Gln Thr Arg Val Asp Lys Leu Thr Gln Gly Arg Gln Thr
 115 120 125
 Tyr Asp Trp Thr Leu Asn Arg Asn Gln Pro Ala Ala Thr Ala Leu Ala
 130 135 140
 Asn Thr Ile Glu Val Phe Arg Ser Asn Gly Leu Thr Ala Asn Glu Ser
 145 150 155 160
 Gly Arg Leu Ile Asp Phe Leu Lys Asp Val Met Glu Ser Met Asn Lys
 165 170 175
 Glu Glu Met Glu Ile Thr Thr His Phe Gln Arg Lys Arg Arg Val Arg
 180 185 190
 Asp Asn Met Thr Lys Lys Met Val Thr Gln Arg Thr Ile Gly Lys Arg
 195 200 205
 Lys Gln Arg Leu Asn Lys Arg Ser Tyr Leu Ile Arg Ala Leu Thr Leu
 210 215 220
 Asn Thr Met Thr Lys Asp Ala Glu Arg Gly Lys Leu Lys Arg Arg Ala
 225 230 235 240
 Ile Ala Thr Pro Gly Met Gln Ile Arg Gly Phe Val Tyr Phe Val Glu
 245 250 255
 Thr Leu Ala Arg Ser Ile Cys Glu Lys Leu Glu Gln Ser Gly Leu Pro
 260 265 270
 Val Gly Gly Asn Glu Lys Lys Ala Lys Leu Ala Asn Val Val Arg Lys
 275 280 285
 Met Met Thr Asn Ser Gln Asp Thr Glu Ile Ser Phe Thr Ile Thr Gly
 290 295 300
 Asp Asn Thr Lys Trp Asn Glu Asn Gln Asn Pro Arg Met Phe Leu Ala
 305 310 315 320
 Met Ile Thr Tyr Ile Thr Arg Asn Gln Pro Glu Trp Phe Arg Asn Val
 325 330 335
 Leu Ser Ile Ala Pro Ile Met Phe Ser Asn Lys Met Ala Arg Leu Gly
 340 345 350
 Lys Gly Tyr Met Phe Glu Ser Lys Ser Met Lys Ile Arg Thr Gln Ile
 355 360 365
 Pro Ala Glu Met Leu Ala Ser Ile Asp Leu Lys Tyr Phe Asn Asp Ser
 370 375 380
 Thr Arg Lys Lys Ile Glu Lys Ile Arg Pro Leu Leu Ile Asp Gly Thr
 385 390 395 400
 Ala Ser Leu Ser Pro Gly Met Met Met Gly Met Phe Asn Met Leu Ser
 405 410 415
 Thr Val Leu Gly Val Ser Ile Leu Asn Leu Gly Gln Lys Arg His Thr
 420 425 430
 Lys Thr Thr Tyr Trp Trp Asp Gly Leu Gln Ser Ser Asp Asp Phe Ala
 435 440 445
 Leu Ile Val Asn Ala Pro Asn His Glu Gly Ile Gln Ala Gly Val Asn
 450 455 460

10073377-000000

Arg Phe Tyr Arg Thr Cys Lys Leu Leu Gly Ile Asn Met Ser Lys Lys
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 Lys Ser Tyr Ile Asn Arg Thr Gly Thr Phe Glu Phe Thr Ser Phe Phe
 485 490 495
 Tyr Arg Tyr Gly Phe Val Ala Asn Phe Ser Met Glu Leu Pro Ser Phe
 500 505 510
 Gly Val Ser Gly Ile Asn Glu Ser Ala Asp Met Ser Ile Gly Val Thr
 515 520 525
 Val Ile Lys Asn Asn Met Ile Asn Asn Asp Leu Gly Pro Ala Thr Ala
 530 535 540
 Gln Met Ala Leu Gln Leu Phe Ile Lys Asp Tyr Arg Tyr Thr Tyr Arg
 545 550 555 560
 Cys His Arg Gly Asp Thr Gln Ile Gln Thr Arg Arg Ser Phe Glu Leu
 565 570 575
 Lys Lys Leu Trp Glu Gln Thr Arg Ser Lys Ala Gly Leu Leu Val Ser
 580 585 590
 Asp Gly Gly Pro Asn Leu Tyr Asn Ile Arg Asn Leu His Ile Pro Glu
 595 600 605
 Val Cys Leu Lys Trp Glu Leu Met Asp Glu Asp Tyr Gln Gly Arg Leu
 610 615 620
 Cys Asn Pro Met Asn Pro Phe Val Ser His Lys Glu Ile Glu Ser Val
 625 630 635 640
 Asn Asn Ala Ala Val Met Pro Ala His Gly Pro Ala Lys Ser Met Glu
 645 650 655
 Tyr Asp Ala Val Ala Thr Thr His Ser Trp Ile Pro Lys Arg Asn Arg
 660 665 670
 Ser Ile Leu Asn Thr Ser Gln Arg Gly Ile Leu Glu Asp Glu Gln Met
 675 680 685
 Tyr Gln Lys Cys Cys Asn Leu Phe Glu Lys Phe Phe Pro Ser Ser Ser
 690 695 700
 Tyr Arg Arg Pro Val Gly Ile Ser Ser Met Val Glu Ala Met Val Ser
 705 710 715 720
 Arg Ala Arg Ile Asp Ala Arg Ile Asp Phe Glu Ser Gly Arg Ile Lys
 725 730 735
 Lys Glu Glu Phe Ala Glu Ile Met Lys Ile Cys Ser Thr Ile Glu Glu
 740 745 750
 Leu Arg Arg Gln Lys
 755

<210> 28

<211> 5169

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: pHL3103

1007337.000000

<400> 28

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acaaagtgtc	gcccggagta	ctggtcgacc	tccgaagttg	gggggggagcg	aaagcaggca	180
aaccatttga	atg gat gtc aat ccg act tta ctg ttc ttg aaa gtt cct					229
	Met Asp Val Asn Pro Thr Leu Leu Phe Leu Lys Val Pro					
	1		5		10	
gcg caa aat gca ata agt act acg ttc cct tac act gga gat cct cca						277
Ala Gln Asn Ala Ile Ser Thr Thr Phe Pro Tyr Thr Gly Asp Pro Pro						
	15		20		25	
tac agc cat gga aca ggg aca gga tac acc atg gac aca gtc aac agg						325
Tyr Ser His Gly Thr Gly Thr Gly Tyr Thr Met Asp Thr Val Asn Arg						
	30		35		40	45
aca cac caa tat tgc gaa aag ggg aaa tgg aca aca aac act gag act						373
Thr His Gln Tyr Ser Glu Lys Gly Lys Trp Thr Thr Asn Thr Glu Thr						
		50			55	60
gga gca ccc caa ctt aat cca att gat ggc cca ttg cct gag gac aat						421
Gly Ala Pro Gln Leu Asn Pro Ile Asp Gly Pro Leu Pro Glu Asp Asn						
		65			70	75
gaa cca agt gga tat gca caa aca gac tgc gtc ctg gaa gca atg gct						469
Glu Pro Ser Gly Tyr Ala Gln Thr Asp Cys Val Leu Glu Ala Met Ala						
	80				85	90
ctc ctt gaa gaa tcc cat cca gga atc ttt gaa aac tgc tgt ctt gag						517
Phe Leu Glu Glu Ser His Pro Gly Ile Phe Glu Asn Ser Cys Leu Glu						
	95				100	105
acg atg gaa gtt gtt caa caa aca aga gtg gac aaa ctg acc caa ggc						565
Thr Met Glu Val Val Gln Gln Thr Arg Val Asp Lys Leu Thr Gln Gly						
	110				115	120
agt cag act tat gat tgg act ttg aat aga aac cag cct gct gca act						613
Arg Gln Thr Tyr Asp Trp Thr Leu Asn Arg Asn Gln Pro Ala Ala Thr						
		130			135	140
ca tta gca aac act ata gag gtc ttt aga tgc aat ggt cta aca gct						661
Ala Leu Ala Asn Thr Ile Glu Val Phe Arg Ser Asn Gly Leu Thr Ala						
		145			150	155
at gaa tca ggg agg ctc ata gat ttc ctc aag gat gtg atg gaa tca						709
asn Glu Ser Gly Arg Leu Ile Asp Phe Leu Lys Asp Val Met Glu Ser						
		160			165	170
tg gat aag gag gaa atg gag ata aca aca cat ttc caa cga aag aga						757
et Asp Lys Glu Glu Met Glu Ile Thr Thr His Phe Gln Arg Lys Arg						
	175				180	185
ga gta aga gac aac atg acc aag aaa atg gtc aca caa aga aca ata						805
arg Val Arg Asp Asn Met Thr Lys Lys Met Val Thr Gln Arg Thr Ile						
	90				195	200
gg aag aaa aag cag aga ctt aac aaa agg agc tac cta ata agg gct						853
ly Lys Lys Lys Gln Arg Leu Asn Lys Arg Ser Tyr Leu Ile Arg Ala						
		210			215	220

cta aca ttg aac aca atg acg aaa gat gca gaa aga ggt aaa ctg aag 901
 Leu Thr Leu Asn Thr Met Thr Lys Asp Ala Glu Arg Gly Lys Leu Lys
 225 230 235

aga aga gca att gca aca cca ggg atg cag atc aga ggg ttt gtg tac 949
 Arg Arg Ala Ile Ala Thr Pro Gly Met Gln Ile Arg Gly Phe Val Tyr
 240 245 250

ttt gtt gag aca ctg gcg aga agc att tgc gag aag ctt gaa cag tct 997
 Phe Val Glu Thr Leu Ala Arg Ser Ile Cys Glu Lys Leu Glu Gln Ser
 255 260 265

ggg cta cca gtt gga ggg aat gag aag aaa gct aaa ttg gca aat gtc 1045
 Gly Leu Pro Val Gly Gly Asn Glu Lys Lys Ala Lys Leu Ala Asn Val
 270 275 280 285

gtg agg aag atg atg acg aac tca caa gac act gag ctc tct ttc aca 1093
 Val Arg Lys Met Met Thr Asn Ser Gln Asp Thr Glu Leu Ser Phe Thr
 290 295 300

atc acc gga gac aat acc aaa tgg aat gag aac caa aac ccc cga atg 1141
 Ile Thr Gly Asp Asn Thr Lys Trp Asn Glu Asn Gln Asn Pro Arg Met
 305 310 315

ttc ctg gca atg ata aca tac atc aca aga aac caa cct gag tgg ttt 1189
 Phe Leu Ala Met Ile Thr Tyr Ile Thr Arg Asn Gln Pro Glu Trp Phe
 320 325 330

aga aat gtc ttg agc atc gcg ccg ata atg ttt tgc aac aaa atg gcg 1237
 Arg Asn Val Leu Ser Ile Ala Pro Ile Met Phe Ser Asn Lys Met Ala
 335 340 345

agg cta ggg aaa ggg tac atg ttc gaa agc aaa agc atg aag ctc cga 1285
 Arg Leu Gly Lys Gly Tyr Met Phe Glu Ser Lys Ser Met Lys Leu Arg
 350 355 360 365

aca caa ata cca gca gaa atg cta gca agt att gat cta aaa tat ttc 1333
 Thr Gln Ile Pro Ala Glu Met Leu Ala Ser Ile Asp Leu Lys Tyr Phe
 370 375 380

aat gaa cca aca agg aag aaa atc gag aaa ata agg cct ctc ata ata 1381
 Asn Glu Pro Thr Arg Lys Lys Ile Glu Lys Ile Arg Pro Leu Ile Ile
 385 390 395

gac ggc aca gcc tca tta agc ccg gga atg atg atg ggt atg ttc aac 1429
 Asp Gly Thr Ala Ser Leu Ser Pro Gly Met Met Met Gly Met Phe Asn
 400 405 410

atg ctg agt aca gtg ttg gga gtc tca atc ctg aat ctt ggg caa aag 1477
 Met Leu Ser Thr Val Leu Gly Val Ser Ile Leu Asn Leu Gly Gln Lys
 415 420 425

aga tac acc aaa acc aca tac tgg tgg gat gga ctt cag tcc tct gat 1525
 Arg Tyr Thr Lys Thr Thr Tyr Trp Trp Asp Gly Leu Gln Ser Ser Asp
 430 435 440 445

gat ttt gct ctc atc gtg aat gca cca aat cat gag gga ata caa gcg 1573
 Asp Phe Ala Leu Ile Val Asn Ala Pro Asn His Glu Gly Ile Gln Ala
 450 455 460

gga gtg gat aga ttc tac aga acc tgc aag cta gtt ggg atc aat atg 1621
 Gly Val Asp Arg Phe Tyr Arg Thr Cys Lys Leu Val Gly Ile Asn Met
 465 470 475

agc aag aaa aag tcc tat ata aat agg aca gga aca ttc gaa ttc aca 1669
 Ser Lys Lys Lys Ser Tyr Ile Asn Arg Thr Gly Thr Phe Glu Phe Thr
 480 485 490

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 Ser Phe Phe Tyr Arg Tyr Gly Phe Val Ala Asn Phe Ser Met Glu Leu
 495 500 505

ccc agc ttt ggg gtg tct ggg atc aac gag tct gcg gac atg agt att 1765
 Pro Ser Phe Gly Val Ser Gly Ile Asn Glu Ser Ala Asp Met Ser Ile
 510 515 520 525

gga gtt act gtc atc aaa aac aat atg ata aac aat gat ctt ggt cca 1813
 Gly Val Thr Val Ile Lys Asn Asn Met Ile Asn Asn Asp Leu Gly Pro
 530 535 540

gca acc gct caa atg gcc ctt cag ctg ttc atc aaa gat tac agg tac 1861
 Ala Thr Ala Gln Met Ala Leu Gln Leu Phe Ile Lys Asp Tyr Arg Tyr
 545 550 555

acg tac cgg tgc cat aga ggt gac aca caa ata caa acc cga aga tca 1909
 Thr Tyr Arg Cys His Arg Gly Asp Thr Gln Ile Gln Thr Arg Arg Ser
 560 565 570

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 Phe Glu Ile Lys Lys Leu Trp Glu Gln Thr His Ser Lys Ala Gly Leu
 575 580 585

ctg gtc tcc gac gga ggc cca aat tta tac aac att aga aat ctc cac 2005
 Leu Val Ser Asp Gly Gly Pro Asn Leu Tyr Asn Ile Arg Asn Leu His
 590 595 600 605

att cct gaa gtc tgc ttg aaa tgg gaa tta atg gat gag gat tac cag 2053
 Ile Pro Glu Val Cys Leu Lys Trp Glu Leu Met Asp Glu Asp Tyr Gln
 610 615 620

ggg cgt tta tgc aac cca ctg aac cca ttt gtc aac cat aaa gac att 2101
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 625 630 635

gaa tca gtg aac aat gca gtg ata atg cca gca cat ggt cca gcc aaa 2149
 Glu Ser Val Asn Asn Ala Val Ile Met Pro Ala His Gly Pro Ala Lys
 640 645 650

aac atg gag tat gat gct gtt gca aca aca cac tcc tgg atc ccc aaa 2197
 Asn Met Glu Tyr Asp Ala Val Ala Thr Thr His Ser Trp Ile Pro Lys
 655 660 665

aga aat cga tcc atc ttg aat aca agc caa aga gga ata ctt gaa gat 2245
 Arg Asn Arg Ser Ile Leu Asn Thr Ser Gln Arg Gly Ile Leu Glu Asp
 670 675 680 685

gaa caa atg tac caa aag tgc tgc aac tta ttt gaa aaa ttc ttc ccc 2293
 Glu Gln Met Tyr Gln Lys Cys Cys Asn Leu Phe Glu Lys Phe Phe Pro
 690 695 700

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 705 710 715

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 720 725 730

agg ata aag aaa gag gag ttc act gag atc atg aag atc tgt tcc acc 2437
 Arg Ile Lys Lys Glu Glu Phe Thr Glu Ile Met Lys Ile Cys Ser Thr
 735 740 745

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 Ile Glu Glu Leu Arg Arg Gln Lys
 750 755

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<211> 757

<212> PRT

<213> Artificial Sequence

<223> Description of Artificial Sequence: pHL3103

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Gly	Thr	Gly	Thr	Gly	Tyr	Thr	Met	Asp	Thr	Val	Asn	Arg	Thr	His	Gln	35	40	45	
Tyr	Ser	Glu	Lys	Gly	Lys	Trp	Thr	Thr	Asn	Thr	Glu	Thr	Gly	Ala	Pro	50	55	60	
Gln	Leu	Asn	Pro	Ile	Asp	Gly	Pro	Leu	Pro	Glu	Asp	Asn	Glu	Pro	Ser	65	70	75	80
Gly	Tyr	Ala	Gln	Thr	Asp	Cys	Val	Leu	Glu	Ala	Met	Ala	Phe	Leu	Glu	85	90	95	
Glu	Ser	His	Pro	Gly	Ile	Phe	Glu	Asn	Ser	Cys	Leu	Glu	Thr	Met	Glu	100	105	110	
Val	Val	Gln	Gln	Thr	Arg	Val	Asp	Lys	Leu	Thr	Gln	Gly	Arg	Gln	Thr	115	120	125	
Tyr	Asp	Trp	Thr	Leu	Asn	Arg	Asn	Gln	Pro	Ala	Ala	Thr	Ala	Leu	Ala	130	135	140	
Asn	Thr	Ile	Glu	Val	Phe	Arg	Ser	Asn	Gly	Leu	Thr	Ala	Asn	Glu	Ser	145	150	155	160
Gly	Arg	Leu	Ile	Asp	Phe	Leu	Lys	Asp	Val	Met	Glu	Ser	Met	Asp	Lys	165	170	175	

Glu Glu Met Glu Ile Thr Thr His Phe Gln Arg Lys Arg Arg Val Arg
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 Asp Asn Met Thr Lys Lys Met Val Thr Gln Arg Thr Ile Gly Lys Lys
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 Lys Gln Arg Leu Asn Lys Arg Ser Tyr Leu Ile Arg Ala Leu Thr Leu
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 Asn Thr Met Thr Lys Asp Ala Glu Arg Gly Lys Leu Lys Arg Arg Ala
 225 230 235 240
 Ile Ala Thr Pro Gly Met Gln Ile Arg Gly Phe Val Tyr Phe Val Glu
 245 250 255
 Thr Leu Ala Arg Ser Ile Cys Glu Lys Leu Glu Gln Ser Gly Leu Pro
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 Val Gly Gly Asn Glu Lys Lys Ala Lys Leu Ala Asn Val Val Arg Lys
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 Asp Asn Thr Lys Trp Asn Glu Asn Gln Asn Pro Arg Met Phe Leu Ala
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 Met Ile Thr Tyr Ile Thr Arg Asn Gln Pro Glu Trp Phe Arg Asn Val
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 Leu Ser Ile Ala Pro Ile Met Phe Ser Asn Lys Met Ala Arg Leu Gly
 340 345 350
 Lys Gly Tyr Met Phe Glu Ser Lys Ser Met Lys Leu Arg Thr Gln Ile
 355 360 365
 Pro Ala Glu Met Leu Ala Ser Ile Asp Leu Lys Tyr Phe Asn Glu Pro
 370 375 380
 Thr Arg Lys Lys Ile Glu Lys Ile Arg Pro Leu Ile Ile Asp Gly Thr
 385 390 395 400
 Ala Ser Leu Ser Pro Gly Met Met Met Gly Met Phe Asn Met Leu Ser
 405 410 415
 Thr Val Leu Gly Val Ser Ile Leu Asn Leu Gly Gln Lys Arg Tyr Thr
 420 425 430
 Lys Thr Thr Tyr Trp Trp Asp Gly Leu Gln Ser Ser Asp Asp Phe Ala
 435 440 445
 Leu Ile Val Asn Ala Pro Asn His Glu Gly Ile Gln Ala Gly Val Asp
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 Arg Phe Tyr Arg Thr Cys Lys Leu Val Gly Ile Asn Met Ser Lys Lys
 465 470 475 480
 Lys Ser Tyr Ile Asn Arg Thr Gly Thr Phe Glu Phe Thr Ser Phe Phe
 485 490 495
 Tyr Arg Tyr Gly Phe Val Ala Asn Phe Ser Met Glu Leu Pro Ser Phe
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 Gly Val Ser Gly Ile Asn Glu Ser Ala Asp Met Ser Ile Gly Val Thr
 515 520 525

1007377-020002

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 545 550 555 560
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 565 570 575
 Lys Lys Leu Trp Glu Gln Thr His Ser Lys Ala Gly Leu Leu Val Ser
 580 585 590
 Asp Gly Gly Pro Asn Leu Tyr Asn Ile Arg Asn Leu His Ile Pro Glu
 595 600 605
 Val Cys Leu Lys Trp Glu Leu Met Asp Glu Asp Tyr Gln Gly Arg Leu
 610 615 620
 Cys Asn Pro Leu Asn Pro Phe Val Asn His Lys Asp Ile Glu Ser Val
 625 630 635 640
 Asn Asn Ala Val Ile Met Pro Ala His Gly Pro Ala Lys Asn Met Glu
 645 650 655
 Tyr Asp Ala Val Ala Thr Thr His Ser Trp Ile Pro Lys Arg Asn Arg
 660 665 670
 Ser Ile Leu Asn Thr Ser Gln Arg Gly Ile Leu Glu Asp Glu Gln Met
 675 680 685
 Tyr Gln Lys Cys Cys Asn Leu Phe Glu Lys Phe Phe Pro Ser Ser Ser
 690 695 700
 Tyr Arg Arg Pro Val Gly Ile Ser Ser Met Val Glu Ala Met Val Ser
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 Arg Ala Arg Ile Asp Ala Arg Ile Asp Phe Glu Ser Gly Arg Ile Lys
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 Leu Arg Arg Gln Lys
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 <212> DNA
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 acaaagtgtc gcccgagta ctggtcgacc tccgaagttg ggggggagcg aaagcaggca 180

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	Met	Asp	Val	Asn	Pro	Thr	Leu	Leu	Phe	Leu	Lys	Val	Pro			
	1				5					10						
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Ala	Gln	Asn	Ala	Ile	Ser	Thr	Thr	Phe	Pro	Tyr	Thr	Gly	Asp	Pro	Pro	
	15				20					25						
tac	agc	cat	ggg	aca	gga	aca	gga	tac	acc	atg	gat	act	gtc	aac	agg	325
Tyr	Ser	His	Gly	Thr	Gly	Thr	Gly	Tyr	Thr	Met	Asp	Thr	Val	Asn	Arg	
	30				35				40						45	
aca	cat	cag	tac	tca	gaa	agg	gga	aga	tgg	aca	aca	aac	acc	gaa	act	373
Thr	His	Gln	Tyr	Ser	Glu	Arg	Gly	Arg	Trp	Thr	Thr	Asn	Thr	Glu	Thr	
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gga	gca	ccg	caa	ctc	aac	ccg	att	gat	ggg	cca	ctg	cca	gaa	gac	aat	421
Gly	Ala	Pro	Gln	Leu	Asn	Pro	Ile	Asp	Gly	Pro	Leu	Pro	Glu	Asp	Asn	
			65				70						75			
gaa	cca	agt	ggt	tat	gcc	caa	aca	gat	tgt	gta	ttg	gaa	gca	atg	gcc	469
Glu	Pro	Ser	Gly	Tyr	Ala	Gln	Thr	Asp	Cys	Val	Leu	Glu	Ala	Met	Ala	
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ttc	ctt	gag	gaa	tcc	cat	cct	ggt	atc	ttt	gag	acc	tcg	tgt	ctt	gaa	517
Phe	Leu	Glu	Glu	Ser	His	Pro	Gly	Ile	Phe	Glu	Thr	Ser	Cys	Leu	Glu	
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acg	atg	gag	gtt	gtt	cag	caa	aca	cga	gtg	gac	aag	ctg	aca	caa	ggc	565
Thr	Met	Glu	Val	Val	Gln	Gln	Thr	Arg	Val	Asp	Lys	Leu	Thr	Gln	Gly	
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Arg	Gln	Thr	Tyr	Asp	Trp	Thr	Leu	Asn	Arg	Asn	Gln	Pro	Ala	Ala	Thr	
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Ala	Leu	Ala	Asn	Thr	Ile	Glu	Val	Phe	Arg	Ser	Asn	Gly	Leu	Thr	Ala	
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Asn	Glu	Ser	Gly	Arg	Leu	Ile	Asp	Phe	Leu	Lys	Asp	Val	Met	Glu	Ser	
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atg	aac	aaa	gaa	gaa	atg	gag	atc	aca	act	cat	ttt	cag	aga	aag	aga	757
Met	Asn	Lys	Glu	Glu	Met	Glu	Ile	Thr	Thr	His	Phe	Gln	Arg	Lys	Arg	
	175					180					185					
cga	gtg	aga	gac	aat	atg	act	aag	aaa	atg	gtg	aca	cag	aga	aca	ata	805
Arg	Val	Arg	Asp	Asn	Met	Thr	Lys	Lys	Met	Val	Thr	Gln	Arg	Thr	Ile	
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gtg Val	agg Arg	aag Lys	atg Met 290	atg Met	acg Thr	aac Asn	tca Ser	caa Gln	gac Asp 295	act Thr	gag Glu	ctc Leu	tct Ser	ttc Phe 300	aca Thr	1093
atc Ile	acc Thr	gga Gly	gac Asp 305	aat Asn	acc Thr	aaa Lys	tgg Trp	aat Asn 310	gag Glu	aac Asn	caa Gln	aac Asn	ccc Pro 315	cga Arg	atg Met	1141
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aat Asn	gaa Glu	cca Pro	aca Thr 385	agg Arg	aag Lys	aaa Lys	atc Ile	gag Glu 390	aaa Lys	ata Ile	agg Arg	cct Pro	ctc Leu 395	ata Ile	ata Ile	1381
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aga Arg 430	tac Tyr	acc Thr	aaa Lys	acc Thr	aca Thr 435	tac Tyr	tgg Trp	tgg Trp	gat Asp	gga Gly 440	ctt Leu	cag Gln	tcc Ser	tct Ser	gat Asp 445	1525
gat Asp	ttt Phe	gct Ala	ctc Leu	atc Ile 450	gtg Val	aat Asn	gca Ala	cca Pro	aat Asn 455	cat His	gag Glu	gga Gly	ata Ile	caa Gln 460	gcg Ala	1573
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agc Ser	ttt Phe 495	ttc Phe	tac Tyr	cgc Arg	tat Tyr	gga Gly 500	ttt Phe	gta Val	gcc Ala	aat Asn 505	ttt Phe	agt Ser	atg Met	gag Glu	ttg Leu	1717
ccc Pro 510	agc Ser	ttt Phe	gga Gly	gta Val 515	tca Ser	gga Gly	att Ile	aat Asn	gaa Glu	tcg Ser 520	gct Ala	gat Asp	atg Met	agc Ser	att Ile 525	1765

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 Ala Thr Ala Gln Met Ala Leu Gln Leu Phe Ile Lys Asp Tyr Arg Tyr
 545 550 555

aca tac agg tgt cac agg gga gac aca caa atc caa acg agg agg tca 1909
 Thr Tyr Arg Cys His Arg Gly Asp Thr Gln Ile Gln Thr Arg Arg Ser
 560 565 570

ttc gag cta aag aag ctg tgg gag cag acc cgc tca aag gca gga ctg 1957
 Phe Glu Leu Lys Lys Leu Trp Glu Gln Thr Arg Ser Lys Ala Gly Leu
 575 580 585

ttg gtt tca gat ggc gga cca aac ctg tac aac att cgg aat ctc cac 2005
 Leu Val Ser Asp Gly Gly Pro Asn Leu Tyr Asn Ile Arg Asn Leu His
 590 595 600 605

atc ccg gaa gtt tgc ctg aaa tgg gaa cta atg gat gaa gac tat cag 2053
 Ile Pro Glu Val Cys Leu Lys Trp Glu Leu Met Asp Glu Asp Tyr Gln
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 Gly Arg Leu Cys Asn Pro Met Asn Pro Phe Val Ser His Lys Glu Ile
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 640 645 650

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 Ser Met Glu Tyr Asp Ala Val Ala Thr Thr His Ser Trp Ile Pro Lys
 655 660 665

aga aac cgt tcc att ctc aat acg agt caa agg gga atc ctt gag gat 2245
 Arg Asn Arg Ser Ile Leu Asn Thr Ser Gln Arg Gly Ile Leu Glu Asp
 670 675 680 685

gaa caa atg tac cag aag tgt tgc aac cta ttc gag aaa ttc ttc cct 2293
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 690 695 700

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 Ser Ser Ser Tyr Arg Arg Pro Val Gly Ile Ser Ser Met Val Glu Ala
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 Met Val Ser Arg Ala Arg Ile Asp Ala Arg Ile Asp Phe Glu Ser Gly
 720 725 730

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 Arg Ile Lys Lys Glu Glu Phe Ala Glu Ile Met Lys Ile Cys Ser Thr
 735 740 745

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<211> 757
<212> PRT
<213> Artificial Sequence
<223> Description of Artificial Sequence: pHL3130
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Tyr	Ser	Glu	Arg	Gly	Arg	Trp	Thr	Thr	Asn	Thr	Glu	Thr	Gly	Ala	Pro
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Gln	Leu	Asn	Pro	Ile	Asp	Gly	Pro	Leu	Pro	Glu	Asp	Asn	Glu	Pro	Ser
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Gly	Tyr	Ala	Gln	Thr	Asp	Cys	Val	Leu	Glu	Ala	Met	Ala	Phe	Leu	Glu
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Glu	Ser	His	Pro	Gly	Ile	Phe	Glu	Thr	Ser	Cys	Leu	Glu	Thr	Met	Glu
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Val	Val	Gln	Gln	Thr	Arg	Val	Asp	Lys	Leu	Thr	Gln	Gly	Arg	Gln	Thr
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Gly	Arg	Leu	Ile	Asp	Phe	Leu	Lys	Asp	Val	Met	Glu	Ser	Met	Asn	Lys
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Glu	Glu	Met	Glu	Ile	Thr	Thr	His	Phe	Gln	Arg	Lys	Arg	Arg	Val	Arg
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Asp	Asn	Met	Thr	Lys	Lys	Met	Val	Thr	Gln	Arg	Thr	Ile	Gly	Lys	Arg
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Lys	Gln	Arg	Leu	Asn	Lys	Arg	Ser	Tyr	Leu	Ile	Arg	Ala	Leu	Thr	Leu
	210					215					220				

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Ile	Ala	Thr	Pro	Gly 245	Met	Gln	Ile	Arg	Gly 250	Phe	Val	Tyr	Phe	Val 255	Glu
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Val	Gly	Gly 275	Asn	Glu	Lys	Lys	Ala 280	Lys	Leu	Ala	Asn	Val 285	Val	Arg	Lys
Met	Met 290	Thr	Asn	Ser	Gln	Asp 295	Thr	Glu	Leu	Ser	Phe 300	Thr	Ile	Thr	Gly
Asp 305	Asn	Thr	Lys	Trp	Asn 310	Glu	Asn	Gln	Asn	Pro 315	Arg	Met	Phe	Leu	Ala 320
Met	Ile	Thr	Tyr	Ile 325	Thr	Arg	Asn	Gln	Pro 330	Glu	Trp	Phe	Arg	Asn 335	Val
Leu	Ser	Ile	Ala 340	Pro	Ile	Met	Phe	Ser 345	Asn	Lys	Met	Ala	Arg 350	Leu	Gly
Lys	Gly	Tyr 355	Met	Phe	Glu	Ser	Lys 360	Ser	Met	Lys	Leu	Arg 365	Thr	Gln	Ile
Pro	Ala 370	Glu	Met	Leu	Ala	Ser 375	Ile	Asp	Leu	Lys	Tyr 380	Phe	Asn	Glu	Pro
Thr 385	Arg	Lys	Lys	Ile	Glu 390	Lys	Ile	Arg	Pro	Leu 395	Ile	Ile	Asp	Gly	Thr 400
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Thr	Val	Leu	Gly 420	Val	Ser	Ile	Leu	Asn 425	Leu	Gly	Gln	Lys	Arg 430	Tyr	Thr
Lys	Thr	Thr 435	Tyr	Trp	Trp	Asp	Gly 440	Leu	Gln	Ser	Ser	Asp 445	Asp	Phe	Ala
Leu	Ile 450	Val	Asn	Ala	Pro	Asn 455	His	Glu	Gly	Ile	Gln 460	Ala	Gly	Val	Asp
Arg 465	Phe	Tyr	Arg	Thr	Cys 470	Lys	Leu	Val	Gly	Ile 475	Asn	Met	Ser	Lys	Lys 480
Lys	Ser	Tyr	Ile	Asn 485	Arg	Thr	Gly	Thr	Phe 490	Glu	Phe	Thr	Ser	Phe 495	Phe
Tyr	Arg	Tyr 500	Gly	Phe	Val	Ala	Asn 505	Phe	Ser	Met	Glu	Leu	Pro 510	Ser	Phe
Gly	Val	Ser 515	Gly	Ile	Asn	Glu	Ser 520	Ala	Asp	Met	Ser	Ile 525	Gly	Val	Thr
Val	Ile 530	Lys	Asn	Asn	Met	Ile 535	Asn	Asn	Asp	Leu	Gly 540	Pro	Ala	Thr	Ala
Gln 545	Met	Ala	Leu	Gln	Leu 550	Phe	Ile	Lys	Asp	Tyr 555	Arg	Tyr	Thr	Tyr	Arg 560
Cys	His	Arg	Gly	Asp 565	Thr	Gln	Ile	Gln	Thr 570	Arg	Arg	Ser	Phe	Glu 575	Leu

Lys Lys Leu Trp Glu Gln Thr Arg Ser Lys Ala Gly Leu Leu Val Ser
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Asp Gly Gly Pro Asn Leu Tyr Asn Ile Arg Asn Leu His Ile Pro Glu
595 600 605

Val Cys Leu Lys Trp Glu Leu Met Asp Glu Asp Tyr Gln Gly Arg Leu
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Cys Asn Pro Met Asn Pro Phe Val Ser His Lys Glu Ile Glu Ser Val
625 630 635 640

Asn Asn Ala Ala Val Met Pro Ala His Gly Pro Ala Lys Ser Met Glu
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Tyr Asp Ala Val Ala Thr Thr His Ser Trp Ile Pro Lys Arg Asn Arg
660 665 670

Ser Ile Leu Asn Thr Ser Gln Arg Gly Ile Leu Glu Asp Glu Gln Met
675 680 685

Tyr Gln Lys Cys Cys Asn Leu Phe Glu Lys Phe Phe Pro Ser Ser Ser
690 695 700

Tyr Arg Arg Pro Val Gly Ile Ser Ser Met Val Glu Ala Met Val Ser
705 710 715 720

Arg Ala Arg Ile Asp Ala Arg Ile Asp Phe Glu Ser Gly Arg Ile Lys
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aaccatttga atg gat gtc aat ccg act tta ctt ttc tta aaa gtg cca 229
Met Asp Val Asn Pro Thr Leu Leu Phe Leu Lys Val Pro
1 5 10
gca caa aat gct ata agc aca act ttc cct tat act gga gac cct cct 277
Ala Gln Asn Ala Ile Ser Thr Thr Phe Pro Tyr Thr Gly Asp Pro Pro
15 20 25
tac agc cat ggg aca gga aca gga tac acc atg gat act gtc aac agg 325
Tyr Ser His Gly Thr Gly Thr Gly Tyr Thr Met Asp Thr Val Asn Arg
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10023322-026800

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Gly	Ala	Pro	Gln	Leu	Asn	Pro	Ile	Asp	Gly	Pro	Leu	Pro	Glu	Asp	Asn	
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gaa	cca	agt	ggt	tat	gcc	caa	aca	gat	tgt	gta	ttg	gaa	gca	atg	gcc	469
Glu	Pro	Ser	Gly	Tyr	Ala	Gln	Thr	Asp	Cys	Val	Leu	Glu	Ala	Met	Ala	
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Phe	Leu	Glu	Glu	Ser	His	Pro	Gly	Ile	Phe	Glu	Thr	Ser	Cys	Leu	Glu	
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Arg	Gln	Thr	Tyr	Asp	Trp	Thr	Leu	Asn	Arg	Asn	Gln	Pro	Ala	Ala	Thr	
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Asn	Glu	Ser	Gly	Arg	Leu	Ile	Asp	Phe	Leu	Lys	Asp	Val	Met	Glu	Ser	
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Met	Asn	Lys	Glu	Glu	Met	Glu	Ile	Thr	Thr	His	Phe	Gln	Arg	Lys	Arg	
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cga	gtg	aga	gac	aat	atg	act	aag	aaa	atg	gtg	aca	cag	aga	aca	ata	805
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Gly	Lys	Arg	Lys	Gln	Arg	Leu	Asn	Lys	Arg	Ser	Tyr	Leu	Ile	Arg	Ala	
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Leu	Thr	Leu	Asn	Thr	Met	Thr	Lys	Asp	Ala	Glu	Arg	Gly	Lys	Leu	Lys	
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Arg	Arg	Ala	Ile	Ala	Thr	Pro	Gly	Met	Gln	Ile	Arg	Gly	Phe	Val	Tyr	
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 aca caa ata cca gca gaa atg cta gca agt att gat cta aaa tat ttc 1333
 Thr Gln Ile Pro Ala Glu Met Leu Ala Ser Ile Asp Leu Lys Tyr Phe
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 Pro Ser Phe Gly Val Ser Gly Ile Asn Glu Ser Ala Asp Met Ser Ile
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 545 550 555
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 Tyr Ser Glu Arg Gly Arg Trp Thr Thr Asn Thr Glu Thr Gly Ala Pro
 50 55 60
 Gln Leu Asn Pro Ile Asp Gly Pro Leu Pro Glu Asp Asn Glu Pro Ser
 65 70 75 80
 Gly Tyr Ala Gln Thr Asp Cys Val Leu Glu Ala Met Ala Phe Leu Glu
 85 90 95
 Glu Ser His Pro Gly Ile Phe Glu Thr Ser Cys Leu Glu Thr Met Glu
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 Val Val Gln Gln Thr Arg Val Asp Lys Leu Thr Gln Gly Arg Gln Thr
 115 120 125
 Tyr Asp Trp Thr Leu Asn Arg Asn Gln Pro Ala Ala Thr Ala Leu Ala
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 145 150 155 160
 Gly Arg Leu Ile Asp Phe Leu Lys Asp Val Met Glu Ser Met Asn Lys
 165 170 175
 Glu Glu Met Glu Ile Thr Thr His Phe Gln Arg Lys Arg Arg Val Arg
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 Asp Asn Met Thr Lys Lys Met Val Thr Gln Arg Thr Ile Gly Lys Arg
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 Lys Gln Arg Leu Asn Lys Arg Ser Tyr Leu Ile Arg Ala Leu Thr Leu
 210 215 220
 Asn Thr Met Thr Lys Asp Ala Glu Arg Gly Lys Leu Lys Arg Arg Ala
 225 230 235 240
 Ile Ala Thr Pro Gly Met Gln Ile Arg Gly Phe Val Tyr Phe Val Glu
 245 250 255
 Thr Leu Ala Arg Ser Ile Cys Glu Lys Leu Glu Gln Ser Gly Leu Pro
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Met	Ile	Thr	Tyr	Ile 325	Thr	Arg	Asn	Gln	Pro 330	Glu	Trp	Phe	Arg	Asn 335
Leu	Ser	Ile	Ala 340	Pro	Ile	Met	Phe	Ser 345	Asn	Lys	Met	Ala	Arg 350	Leu 355
Lys	Gly	Tyr	Met 355	Phe	Glu	Ser	Lys 360	Ser	Met	Lys	Leu	Arg 365	Thr	Gln 370
Pro 370	Ala	Glu	Met	Leu	Ala	Ser 375	Ile	Asp	Leu	Lys	Tyr 380	Phe	Asn	Glu 385
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Thr	Val	Leu	Gly 420	Val	Ser	Ile	Leu	Asn 425	Leu	Gly	Gln	Lys	Arg 430	Tyr 435
Lys	Thr	Thr	Tyr 435	Trp	Trp	Asp	Gly 440	Leu	Gln	Ser	Ser	Asp 445	Asp	Phe 450
Leu 450	Ile	Val	Asn	Ala	Pro	Asn 455	His	Glu	Gly	Ile	Gln 460	Ala	Gly	Val 465
Arg 465	Phe	Tyr	Arg	Thr	Cys 470	Lys	Leu	Val	Gly	Ile 475	Asn	Met	Ser	Lys 480
Lys	Ser	Tyr	Ile	Asn 485	Arg	Thr	Gly	Thr	Phe 490	Glu	Phe	Thr	Ser	Phe 495
Tyr	Arg	Tyr	Gly 500	Phe	Val	Ala	Asn 505	Phe	Ser	Met	Glu	Leu	Pro 510	Ser 515
Gly	Val	Ser 515	Gly	Ile	Asn	Glu	Ser 520	Ala	Asp	Met	Ser	Ile 525	Gly	Val 530
Val 530	Ile	Lys	Asn	Asn	Met	Ile 535	Asn	Asn	Asp	Leu	Gly 540	Pro	Ala	Thr 545
Gln 545	Met	Ala	Leu	Gln	Leu 550	Phe	Ile	Lys	Asp	Tyr 555	Arg	Tyr	Thr	Tyr 560
Cys	His	Arg	Gly	Asp 565	Thr	Gln	Ile	Gln	Thr 570	Arg	Arg	Ser	Phe	Glu 575
Lys	Lys	Leu	Trp 580	Glu	Gln	Thr	His	Ser 585	Lys	Ala	Gly	Leu	Leu 590	Val 595
Asp	Gly	Gly 595	Pro	Asn	Leu	Tyr	Asn 600	Ile	Arg	Asn	Leu	His 605	Ile	Pro 610
Val 610	Cys	Leu	Lys	Trp	Glu	Leu 615	Met	Asp	Glu	Asp	Tyr 620	Gln	Gly	Arg 625
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Asn	Glu	Ser	Gly	Arg	Leu	Ile	Asp	Phe	Leu	Lys	Asp	Val	Met	Glu	Ser	
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Arg	Val	Arg	Asp	Asn	Met	Thr	Lys	Lys	Met	Val	Thr	Gln	Arg	Thr	Ile	
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Gly	Lys	Arg	Lys	Gln	Arg	Leu	Asn	Lys	Arg	Ser	Tyr	Leu	Ile	Arg	Ala	
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Phe	Val	Glu	Thr	Leu	Ala	Arg	Ser	Ile	Cys	Glu	Lys	Leu	Glu	Gln	Ser	
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 Thr Gln Ile Pro Ala Glu Met Leu Ala Ser Ile Asp Leu Lys Tyr Phe 380
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 Thr Tyr Arg Cys His Arg Gly Asp Thr Gln Ile Gln Thr Arg Arg Ser 570
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ctg gtc tcc gac gga gcc cca aat ttg tac aac att cgg aat ctc cac 2005
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35 40 45

Tyr Ser Glu Arg Gly Arg Trp Thr Thr Asn Thr Glu Thr Gly Ala Pro
50 55 60

Gln Leu Asn Pro Ile Asp Gly Pro Leu Pro Glu Asp Asn Glu Pro Ser
65 70 75 80

Gly Tyr Ala Gln Thr Asp Cys Val Leu Glu Ala Met Ala Phe Leu Glu
85 90 95

Glu Ser His Pro Gly Ile Phe Glu Thr Ser Cys Leu Glu Thr Met Glu
100 105 110

Val Val Gln Gln Thr Arg Val Asp Lys Leu Thr Gln Gly Arg Gln Thr
115 120 125

Tyr Asp Trp Thr Leu Asn Arg Asn Gln Pro Ala Ala Thr Ala Leu Ala
130 135 140

Asn Thr Ile Glu Val Phe Arg Ser Asn Gly Leu Thr Ala Asn Glu Ser
145 150 155 160

Gly Arg Leu Ile Asp Phe Leu Lys Asp Val Met Glu Ser Met Asn Lys
165 170 175

Glu Glu Met Glu Ile Thr Thr His Phe Gln Arg Lys Arg Arg Val Arg
180 185 190

Asp Asn Met Thr Lys Lys Met Val Thr Gln Arg Thr Ile Gly Lys Arg
195 200 205

Lys Gln Arg Leu Asn Lys Arg Ser Tyr Leu Ile Arg Ala Leu Thr Leu
210 215 220

Asn Thr Met Thr Lys Asp Ala Glu Arg Gly Lys Leu Lys Arg Arg Ala
225 230 235 240

Ile Ala Thr Pro Gly Met Gln Ile Arg Gly Phe Val Tyr Phe Val Glu
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Thr Leu Ala Arg Ser Ile Cys Glu Lys Leu Glu Gln Ser Gly Leu Pro
260 265 270

Val Gly Gly Asn Glu Lys Lys Ala Lys Leu Ala Asn Val Val Arg Lys
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Asp Asn Thr Lys Trp Asn Glu Asn Gln Asn Pro Arg Met Phe Leu Ala
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Leu Ser Ile Ala Pro Ile Met Phe Ser Asn Lys Met Ala Arg Leu Gly
340 345 350

1007337-000000

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Ser	Ile	Leu	Asn	Thr	Ser	Gln	Arg	Gly	Ile	Leu	Glu	Asp	Glu	Gln	Met	675	680	685
Tyr	Gln	Lys	Cys	Cys	Asn	Leu	Phe	Glu	Lys	Phe	Phe	Pro	Ser	Ser	Ser	690	695	700

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Arg Ala Arg Ile Asp Ala Arg Ile Asp Phe Glu Ser Gly Arg Ile Lys
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aggatcttca cctagatcct tttaaattaa aaatgaagtt ttaaataaat cttaaagtata 3751

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<211> 757

<212> PRT

<213> Artificial Sequence

<223> Description of Artificial Sequence: pHL3204

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Gly	Thr	Gly	Thr	Gly	Tyr	Thr	Met	Asp	Thr	Val	Asn	Arg	Thr	His	Gln
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Tyr	Ser	Glu	Arg	Gly	Arg	Trp	Thr	Thr	Asn	Thr	Glu	Thr	Gly	Ala	Pro
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Gln Leu Asn Pro Ile Asp Gly Pro Leu Pro Glu Asp Asn Glu Pro Ser
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 Gly Tyr Ala Gln Thr Asp Cys Val Leu Glu Ala Met Ala Phe Leu Glu
 85 90 95
 Glu Ser His Pro Gly Ile Phe Glu Thr Ser Cys Leu Glu Thr Met Glu
 100 105 110
 Val Val Gln Gln Thr Arg Val Asp Lys Leu Thr Gln Gly Arg Gln Thr
 115 120 125
 Tyr Asp Trp Thr Leu Asn Arg Asn Gln Pro Ala Ala Thr Ala Leu Ala
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 Asn Thr Ile Glu Val Phe Arg Ser Asn Gly Leu Thr Ala Asn Glu Ser
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 Gly Arg Leu Ile Asp Phe Leu Lys Asp Val Met Glu Ser Met Asn Lys
 165 170 175
 Glu Glu Met Glu Ile Thr Thr His Phe Gln Arg Lys Arg Arg Val Arg
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 Asp Asn Met Thr Lys Lys Met Val Thr Gln Arg Thr Ile Gly Lys Arg
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 Lys Gln Arg Leu Asn Lys Arg Ser Tyr Leu Ile Arg Ala Leu Thr Leu
 210 215 220
 Asn Thr Met Thr Lys Asp Ala Glu Arg Gly Lys Leu Lys Arg Arg Ala
 225 230 235 240
 Ile Ala Thr Pro Gly Met Gln Ile Arg Gly Phe Val Tyr Phe Val Glu
 245 250 255
 Thr Leu Ala Arg Ser Ile Cys Glu Lys Leu Glu Gln Ser Gly Leu Pro
 260 265 270
 Val Gly Gly Asn Glu Lys Lys Ala Lys Leu Ala Asn Val Val Arg Lys
 275 280 285
 Met Met Thr Asn Ser Gln Asp Thr Glu Ile Ser Phe Thr Ile Thr Gly
 290 295 300
 Asp Asn Thr Lys Trp Asn Glu Asn Gln Asn Pro Arg Met Phe Leu Ala
 305 310 315 320
 Met Ile Thr Tyr Ile Thr Arg Asn Gln Pro Glu Trp Phe Arg Asn Val
 325 330 335
 Leu Ser Ile Ala Pro Ile Met Phe Ser Asn Lys Met Ala Arg Leu Gly
 340 345 350
 Lys Gly Tyr Met Phe Glu Ser Lys Ser Met Lys Ile Arg Thr Gln Ile
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 Pro Ala Glu Met Leu Ala Ser Ile Asp Leu Lys Tyr Phe Asn Asp Ser
 370 375 380
 Thr Arg Lys Lys Ile Glu Lys Ile Arg Pro Leu Leu Ile Asp Gly Thr
 385 390 395 400
 Ala Ser Leu Ser Pro Gly Met Met Met Gly Met Phe Asn Met Leu Ser
 405 410 415

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Thr Val Leu Gly Val Ser Ile Leu Asn Leu Gly Gln Lys Arg His Thr
 420 425 430
 Lys Thr Thr Tyr Trp Trp Asp Gly Leu Gln Ser Ser Asp Asp Phe Ala
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 Leu Ile Val Asn Ala Pro Asn His Glu Gly Ile Gln Ala Gly Val Asn
 450 455 460
 Arg Phe Tyr Arg Thr Cys Lys Leu Leu Gly Ile Asn Met Ser Lys Lys
 465 470 475 480
 Lys Ser Tyr Ile Asn Arg Thr Gly Thr Phe Glu Phe Thr Ser Phe Phe
 485 490 495
 Tyr Arg Tyr Gly Phe Val Ala Asn Phe Ser Met Glu Leu Pro Ser Phe
 500 505 510
 Gly Val Ser Gly Ile Asn Glu Ser Ala Asp Met Ser Ile Gly Val Thr
 515 520 525
 Val Ile Lys Asn Asn Met Ile Asn Asn Asp Leu Gly Pro Ala Thr Ala
 530 535 540
 Gln Met Ala Leu Gln Leu Phe Ile Lys Asp Tyr Arg Tyr Thr Tyr Arg
 545 550 555 560
 Cys His Arg Gly Asp Thr Gln Ile Gln Thr Arg Arg Ser Phe Glu Leu
 565 570 575
 Lys Lys Leu Trp Glu Gln Thr Arg Ser Lys Ala Gly Leu Leu Val Ser
 580 585 590
 Asp Gly Gly Pro Asn Leu Tyr Asn Ile Arg Asn Leu His Ile Pro Glu
 595 600 605
 Val Cys Leu Lys Trp Glu Leu Met Asp Glu Asp Tyr Gln Gly Arg Leu
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 Cys Asn Pro Leu Asn Pro Phe Val Asn His Lys Asp Ile Glu Ser Val
 625 630 635 640
 Asn Asn Ala Val Ile Met Pro Ala His Gly Pro Ala Lys Asn Met Glu
 645 650 655
 Tyr Asp Ala Val Ala Thr Thr His Ser Trp Ile Pro Lys Arg Asn Arg
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 Tyr Gln Lys Cys Cys Asn Leu Phe Glu Lys Phe Phe Pro Ser Ser Ser
 690 695 700
 Tyr Arg Arg Pro Val Gly Ile Ser Ser Met Val Glu Ala Met Val Ser
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 Arg Ala Arg Ile Asp Ala Arg Ile Asp Phe Glu Ser Gly Arg Ile Lys
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 Lys Glu Glu Phe Thr Glu Ile Met Lys Ile Cys Ser Thr Ile Glu Glu
 740 745 750
 Leu Arg Arg Gln Lys
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Gly	Lys	Arg	Lys	Gln	Arg	Leu	Asn	Lys	Arg	Ser	Tyr	Leu	Ile	Arg	Ala	
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tta	acc	ctg	aac	aca	atg	acc	aaa	gat	gct	gag	aga	ggg	aag	cta	aaa	901
Leu	Thr	Leu	Asn	Thr	Met	Thr	Lys	Asp	Ala	Glu	Arg	Gly	Lys	Leu	Lys	
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Arg	Arg	Ala	Ile	Ala	Thr	Pro	Gly	Met	Gln	Ile	Arg	Gly	Phe	Val	Tyr	
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Phe	Val	Glu	Thr	Leu	Ala	Arg	Ser	Ile	Cys	Glu	Lys	Leu	Glu	Gln	Ser	
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gtg	agg	aag	atg	atg	acg	aac	tca	caa	gac	act	gag	ctc	tct	ttc	aca	1093
Val	Arg	Lys	Met	Met	Thr	Asn	Ser	Gln	Asp	Thr	Glu	Leu	Ser	Phe	Thr	
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atc	acc	gga	gac	aat	acc	aaa	tgg	aat	gag	aac	caa	aac	ccc	cga	atg	1141
Ile	Thr	Gly	Asp	Asn	Thr	Lys	Trp	Asn	Glu	Asn	Gln	Asn	Pro	Arg	Met	
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Phe	Leu	Ala	Met	Ile	Thr	Tyr	Ile	Thr	Arg	Asn	Gln	Pro	Glu	Trp	Phe	
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Arg	Asn	Val	Leu	Ser	Ile	Ala	Pro	Ile	Met	Phe	Ser	Asn	Lys	Met	Ala	
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agg	cta	ggg	aaa	ggg	tac	atg	ttc	gaa	agc	aaa	agc	atg	aag	ctc	cga	1285
Arg	Leu	Gly	Lys	Gly	Tyr	Met	Phe	Glu	Ser	Lys	Ser	Met	Lys	Leu	Arg	
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aca	caa	ata	cca	gca	gaa	atg	cta	gca	agc	atc	gat	ttg	aaa	tac	ttc	1333
Thr	Gln	Ile	Pro	Ala	Glu	Met	Leu	Ala	Ser	Ile	Asp	Leu	Lys	Tyr	Phe	
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aat	gat	tca	act	aga	aag	aag	att	gaa	aaa	atc	cgg	ccg	ctc	tta	ata	1381
Asn	Asp	Ser	Thr	Arg	Lys	Lys	Ile	Glu	Lys	Ile	Arg	Pro	Leu	Leu	Ile	
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gat	ggg	act														

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480 485 490	
agc ttt ttc tat cgt tat ggg ttt gtt gcc aat ttc agc atg gag ctt Ser Phe Phe Tyr Arg Tyr Gly Phe Val Ala Asn Phe Ser Met Glu Leu	1717
495 500 505	
ccc agc ttt ggg gtg tct ggg atc aac gag tct gcg gac atg agt att Pro Ser Phe Gly Val Ser Gly Ile Asn Glu Ser Ala Asp Met Ser Ile	1765
510 515 520 525	
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575 580 585	
ctg gtc tcc gac gga ggc cca aat tta tac aac att aga aat ctc cac Leu Val Ser Asp Gly Gly Pro Asn Leu Tyr Asn Ile Arg Asn Leu His	2005
590 595 600 605	
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625 630 635	
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640 645 650	
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655 660 665	
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670 675 680 685	
gaa caa atg tac caa aag tgc tgc aac tta ttt gaa aaa ttc ttc ccc Glu Gln Met Tyr Gln Lys Cys Cys Asn Leu Phe Glu Lys Phe Phe Pro	2293
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<223> Description of Artificial Sequence: pHL3246
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Gly Thr Gly Thr Gly Tyr Thr Met Asp Thr Val Asn Arg Thr His Gln
35 40 45

Tyr Ser Glu Arg Gly Arg Trp Thr Thr Asn Thr Glu Thr Gly Ala Pro
50 55 60

Gln Leu Asn Pro Ile Asp Gly Pro Leu Pro Glu Asp Asn Glu Pro Ser
65 70 75 80

Gly Tyr Ala Gln Thr Asp Cys Val Leu Glu Ala Met Ala Phe Leu Glu
85 90 95

Glu Ser His Pro Gly Ile Phe Glu Thr Ser Cys Leu Glu Thr Met Glu
100 105 110

Val Val Gln Gln Thr Arg Val Asp Lys Leu Thr Gln Gly Arg Gln Thr
115 120 125

Tyr Asp Trp Thr Leu Asn Arg Asn Gln Pro Ala Ala Thr Ala Leu Ala
 130 135 140
 Asn Thr Ile Glu Val Phe Arg Ser Asn Gly Leu Thr Ala Asn Glu Ser
 145 150 155 160
 Gly Arg Leu Ile Asp Phe Leu Lys Asp Val Met Glu Ser Met Asn Lys
 165 170 175
 Glu Glu Met Glu Ile Thr Thr His Phe Gln Arg Lys Arg Arg Val Arg
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 Asp Asn Met Thr Lys Lys Met Val Thr Gln Arg Thr Ile Gly Lys Arg
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 Lys Gln Arg Leu Asn Lys Arg Ser Tyr Leu Ile Arg Ala Leu Thr Leu
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 Asn Thr Met Thr Lys Asp Ala Glu Arg Gly Lys Leu Lys Arg Arg Ala
 225 230 235 240
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 Thr Leu Ala Arg Ser Ile Cys Glu Lys Leu Glu Gln Ser Gly Leu Pro
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 Val Gly Gly Asn Glu Lys Lys Ala Lys Leu Ala Asn Val Val Arg Lys
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 Met Met Thr Asn Ser Gln Asp Thr Glu Leu Ser Phe Thr Ile Thr Gly
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 Asp Asn Thr Lys Trp Asn Glu Asn Gln Asn Pro Arg Met Phe Leu Ala
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 325 330 335
 Leu Ser Ile Ala Pro Ile Met Phe Ser Asn Lys Met Ala Arg Leu Gly
 340 345 350
 Lys Gly Tyr Met Phe Glu Ser Lys Ser Met Lys Leu Arg Thr Gln Ile
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 Pro Ala Glu Met Leu Ala Ser Ile Asp Leu Lys Tyr Phe Asn Asp Ser
 370 375 380
 Thr Arg Lys Lys Ile Glu Lys Ile Arg Pro Leu Leu Ile Asp Gly Thr
 385 390 395 400
 Ala Ser Leu Ser Pro Gly Met Met Met Gly Met Phe Asn Met Leu Ser
 405 410 415
 Thr Val Leu Gly Val Ser Ile Leu Asn Leu Gly Gln Lys Arg His Thr
 420 425 430
 Lys Thr Thr Tyr Trp Trp Asp Gly Leu Gln Ser Ser Asp Asp Phe Ala
 435 440 445
 Leu Ile Val Asn Ala Pro Asn His Glu Gly Ile Gln Ala Gly Val Asn
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 Arg Phe Tyr Arg Thr Cys Lys Leu Leu Gly Ile Asn Met Ser Lys Lys
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Lys Ser Tyr Ile Asn Arg Thr Gly Thr Phe Glu Phe Thr Ser Phe Phe
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 515 520 525
 Val Ile Lys Asn Asn Met Ile Asn Asn Asp Leu Gly Pro Ala Thr Ala
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 Gln Met Ala Leu Gln Leu Phe Ile Lys Asp Tyr Arg Tyr Thr Tyr Arg
 545 550 555 560
 Cys His Arg Gly Asp Thr Gln Ile Gln Thr Arg Arg Ser Phe Glu Ile
 565 570 575
 Lys Lys Leu Trp Glu Gln Thr His Ser Lys Ala Gly Leu Leu Val Ser
 580 585 590
 Asp Gly Gly Pro Asn Leu Tyr Asn Ile Arg Asn Leu His Ile Pro Glu
 595 600 605
 Val Cys Leu Lys Trp Glu Leu Met Asp Glu Asp Tyr Gln Gly Arg Leu
 610 615 620
 Cys Asn Pro Leu Asn Pro Phe Val Asn His Lys Asp Ile Glu Ser Val
 625 630 635 640
 Asn Asn Ala Val Ile Met Pro Ala His Gly Pro Ala Lys Asn Met Glu
 645 650 655
 Tyr Asp Ala Val Ala Thr Thr His Ser Trp Ile Pro Lys Arg Asn Arg
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 675 680 685
 Tyr Gln Lys Cys Cys Asn Leu Phe Glu Lys Phe Phe Pro Ser Ser Ser
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 Tyr Arg Arg Pro Val Gly Ile Ser Ser Met Val Glu Ala Met Val Ser
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aaccatttga atg gat gtc aat ccg act tta ctt ttc tta aaa gtg cca 229
 Met Asp Val Asn Pro Thr Leu Leu Phe Leu Lys Val Pro
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 Ala Gln Asn Ala Ile Ser Thr Thr Phe Pro Tyr Thr Gly Asp Pro Pro
 15 20 25

tac agc cat ggg aca gga aca gga tac acc atg gat act gtc aac agg 325
 Tyr Ser His Gly Thr Gly Thr Gly Tyr Thr Met Asp Thr Val Asn Arg
 30 35 40 45

aca cat cag tac tca gaa agg gga aga tgg aca aca aac acc gaa act 373
 Thr His Gln Tyr Ser Glu Arg Gly Arg Trp Thr Thr Asn Thr Glu Thr
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 Glu Pro Ser Gly Tyr Ala Gln Thr Asp Cys Val Leu Glu Ala Met Ala
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 Phe Leu Glu Glu Ser His Pro Gly Ile Phe Glu Thr Ser Cys Leu Glu
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acg atg gag gtt gtt cag caa aca cga gtg gac aag ctg aca caa ggc 565
 Thr Met Glu Val Val Gln Gln Thr Arg Val Asp Lys Leu Thr Gln Gly
 110 115 120 125

cga cag acc tat gac tgg act cta aat agg aac cag cct gct gca aca 613
 Arg Gln Thr Tyr Asp Trp Thr Leu Asn Arg Asn Gln Pro Ala Ala Thr
 130 135 140

gca ttg gcc aac aca ata gaa gtg ttc aga tca aat ggc ctc acg gcc 661
 Ala Leu Ala Asn Thr Ile Glu Val Phe Arg Ser Asn Gly Leu Thr Ala
 145 150 155

aat gaa tct gga agg ctc ata gac ttc ctt aag gat gta atg gag tca 709
 Asn Glu Ser Gly Arg Leu Ile Asp Phe Leu Lys Asp Val Met Glu Ser
 160 165 170

atg aac aaa gaa gaa atg gag atc aca act cat ttt cag aga aag aga 757
 Met Asn Lys Glu Glu Met Glu Ile Thr Thr His Phe Gln Arg Lys Arg
 175 180 185

cga gtg aga gac aat atg act aag aaa atg gtg aca cag aga aca ata 805
 Arg Val Arg Asp Asn Met Thr Lys Lys Met Val Thr Gln Arg Thr Ile
 190 195 200 205

ggt aaa agg aag cag aga ttg aac aaa agg agt tat cta att agg gca 853
 Gly Lys Arg Lys Gln Arg Leu Asn Lys Arg Ser Tyr Leu Ile Arg Ala
 210 215 220

tta acc ctg aac aca atg acc aaa gat gct gag aga ggg aag cta aaa 901
 Leu Thr Leu Asn Thr Met Thr Lys Asp Ala Glu Arg Gly Lys Leu Lys
 225 230 235

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 Arg Arg Ala Ile Ala Thr Pro Gly Met Gln Ile Arg Gly Phe Val Tyr
 240 245 250

ttt gtt gag aca cta gca agg agt ata tgt gag aaa ctt gaa caa tca 997
 Phe Val Glu Thr Leu Ala Arg Ser Ile Cys Glu Lys Leu Glu Gln Ser
 255 260 265

gga ttg cca gtt gga ggc aat gag aag aaa gca aag ttg gca aat gtt 1045
 Gly Leu Pro Val Gly Gly Asn Glu Lys Lys Ala Lys Leu Ala Asn Val
 270 275 280 285

gta agg aag atg atg acc aat tct cag gac act gaa att tct ttc acc 1093
 Val Arg Lys Met Met Thr Asn Ser Gln Asp Thr Glu Ile Ser Phe Thr
 290 295 300

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 Ile Thr Gly Asp Asn Thr Lys Trp Asn Glu Asn Gln Asn Pro Arg Met
 305 310 315

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 Phe Leu Ala Met Ile Thr Tyr Ile Thr Arg Asn Gln Pro Glu Trp Phe
 320 325 330

aga aat gtt cta agt att gct cca ata atg ttc tca aac aaa atg gcg 1237
 Arg Asn Val Leu Ser Ile Ala Pro Ile Met Phe Ser Asn Lys Met Ala
 335 340 345

aga ctg gga aag ggg tac atg ttt gag agc aag agt atg aaa att aga 1285
 Arg Leu Gly Lys Gly Tyr Met Phe Glu Ser Lys Ser Met Lys Ile Arg
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act caa ata cct gca gaa atg cta gca agt att gat cta aaa tat ttc 1333
 Thr Gln Ile Pro Ala Glu Met Leu Ala Ser Ile Asp Leu Lys Tyr Phe
 370 375 380

aat gaa cca aca agg aag aaa atc gag aaa ata agg cct ctc ata ata 1381
 Asn Glu Pro Thr Arg Lys Lys Ile Glu Lys Ile Arg Pro Leu Ile Ile
 385 390 395

gac ggc aca gcc tca tta agc ccg gga atg atg atg ggt atg ttc aac 1429
 Asp Gly Thr Ala Ser Leu Ser Pro Gly Met Met Met Gly Met Phe Asn
 400 405 410

atg ctg agt aca gtg ttg gga gtc tca atc ctg aat ctt ggg caa aag 1477
 Met Leu Ser Thr Val Leu Gly Val Ser Ile Leu Asn Leu Gly Gln Lys
 415 420 425

aga tac acc aaa acc aca tac tgg tgg gat gga ctt cag tcc tct gat 1525
 Arg Tyr Thr Lys Thr Thr Tyr Trp Trp Asp Gly Leu Gln Ser Ser Asp
 430 435 440 445

gat ttt gct ctc atc gtg aat gca cca aat cat gag gga ata caa gcg 1573
 Asp Phe Ala Leu Ile Val Asn Ala Pro Asn His Glu Gly Ile Gln Ala
 450 455 460

gga gtg gat aga ttc tac aga acc tgc aag cta gtt ggg atc aat atg 1621
 Gly Val Asp Arg Phe Tyr Arg Thr Cys Lys Leu Val Gly Ile Asn Met
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 Ser Lys Lys Lys Ser Tyr Ile Asn Arg Thr Gly Thr Phe Glu Phe Thr
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1007337-823300

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ccc Pro 510	agc Ser	ttt Phe	ggg Gly	gtg Val	tct Ser 515	ggg Gly	atc Ile	aac Asn	gag Glu	tct Ser 520	gcg Ala	gac Asp	atg Met	agt Ser	att Ile 525	1765
gga Gly	gtt Val	act Thr	gtc Val	atc Ile 530	aaa Lys	aac Asn	aat Asn	atg Met	ata Ile 535	aac Asn	aat Asn	gat Asp	ctt Leu	ggt Gly 540	cca Pro	1813
gca Ala	acc Thr	gct Ala	caa Gln 545	atg Met	gcc Ala	ctt Leu	cag Gln	ctg Leu 550	ttc Phe	atc Ile	aaa Lys	gat Asp	tac Tyr 555	agg Arg	tac Tyr	1861
acg Thr	tac Tyr	cgg Arg 560	tgc Cys	cat His	aga Arg	ggg Gly	gac Asp 565	aca Thr	caa Gln	ata Ile	caa Gln	acc Thr 570	cga Arg	aga Arg	tca Ser	1909
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ctg Leu 590	gtc Val	tcc Ser	gac Asp	gga Gly	ggc Gly 595	cca Pro	aat Asn	tta Leu	tac Tyr	aac Asn 600	att Ile	aga Arg	aat Asn	ctc Leu	cac His 605	2005
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ggg Gly	cgt Arg	tta Leu	tgc Cys 625	aac Asn	cca Pro	ctg Leu	aac Asn	cca Pro 630	ttt Phe	gtc Val	aac Asn	cat His	aaa Lys 635	gac Asp	att Ile	2101
gaa Glu	tca Ser	gtg Val 640	aac Asn	aat Asn	gca Ala	gtg Val	ata Ile 645	atg Met	cca Pro	gca Ala	cat His	ggt Gly 650	cca Pro	gcc Ala	aaa Lys	2149
aac Asn 655	atg Met	gag Glu	tat Tyr	gat Asp	gct Ala	gtt Val 660	gca Ala	aca Thr	aca Thr	cac His	tcc Ser 665	tgg Trp	atc Ile	ccc Pro	aaa Lys	2197
aga Arg 670	aat Asn	cga Arg	tcc Ser	atc Ile	ttg Leu 675	aat Asn	aca Thr	agc Ser	caa Gln	aga Arg 680	gga Gly	ata Ile	ctt Leu	gaa Glu	gat Asp 685	2245
gaa Glu	caa Gln	atg Met	tac Tyr	caa Gln 690	aag Lys	tgc Cys	tgc Cys	aac Asn	tta Leu 695	ttt Phe	gaa Glu	aaa Lys	ttc Phe	ttc Phe 700	ccc Pro	2293
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atg Met	gtt Val	tcc Ser	aga Arg	gcc Ala	cga Arg	att Ile	gat Asp 725	gca Ala	cga Arg	att Ile	gat Asp	ttc Phe 730	gaa Glu	tct Ser	gga Gly	2389
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Gly Thr Gly Thr Gly Tyr Thr Met Asp Thr Val Asn Arg Thr His Gln
35 40 45
Tyr Ser Glu Arg Gly Arg Trp Thr Thr Asn Thr Glu Thr Gly Ala Pro
50 55 60
Gln Leu Asn Pro Ile Asp Gly Pro Leu Pro Glu Asp Asn Glu Pro Ser
65 70 75 80
Gly Tyr Ala Gln Thr Asp Cys Val Leu Glu Ala Met Ala Phe Leu Glu
85 90 95
Glu Ser His Pro Gly Ile Phe Glu Thr Ser Cys Leu Glu Thr Met Glu
100 105 110
Val Val Gln Gln Thr Arg Val Asp Lys Leu Thr Gln Gly Arg Gln Thr
115 120 125
Tyr Asp Trp Thr Leu Asn Arg Asn Gln Pro Ala Ala Thr Ala Leu Ala
130 135 140
Asn Thr Ile Glu Val Phe Arg Ser Asn Gly Leu Thr Ala Asn Glu Ser
145 150 155 160
Gly Arg Leu Ile Asp Phe Leu Lys Asp Val Met Glu Ser Met Asn Lys
165 170 175
Glu Glu Met Glu Ile Thr Thr His Phe Gln Arg Lys Arg Arg Val Arg
180 185 190

10073377-020002

Asp	Asn	Met	Thr	Lys	Lys	Met	Val	Thr	Gln	Arg	Thr	Ile	Gly	Lys	Arg
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Lys	Gln	Arg	Leu	Asn	Lys	Arg	Ser	Tyr	Leu	Ile	Arg	Ala	Leu	Thr	Leu
210					215						220				
Asn	Thr	Met	Thr	Lys	Asp	Ala	Glu	Arg	Gly	Lys	Leu	Lys	Arg	Arg	Ala
225				230						235					240
Ile	Ala	Thr	Pro	Gly	Met	Gln	Ile	Arg	Gly	Phe	Val	Tyr	Phe	Val	Glu
				245					250					255	
Thr	Leu	Ala	Arg	Ser	Ile	Cys	Glu	Lys	Leu	Glu	Gln	Ser	Gly	Leu	Pro
			260					265					270		
Val	Gly	Gly	Asn	Glu	Lys	Lys	Ala	Lys	Leu	Ala	Asn	Val	Val	Arg	Lys
	275						280					285			
Met	Met	Thr	Asn	Ser	Gln	Asp	Thr	Glu	Ile	Ser	Phe	Thr	Ile	Thr	Gly
290						295					300				
Asp	Asn	Thr	Lys	Trp	Asn	Glu	Asn	Gln	Asn	Pro	Arg	Met	Phe	Leu	Ala
305					310					315					320
Met	Ile	Thr	Tyr	Ile	Thr	Arg	Asn	Gln	Pro	Glu	Trp	Phe	Arg	Asn	Val
				325					330					335	
Leu	Ser	Ile	Ala	Pro	Ile	Met	Phe	Ser	Asn	Lys	Met	Ala	Arg	Leu	Gly
			340					345					350		
Lys	Gly	Tyr	Met	Phe	Glu	Ser	Lys	Ser	Met	Lys	Ile	Arg	Thr	Gln	Ile
		355					360					365			
Pro	Ala	Glu	Met	Leu	Ala	Ser	Ile	Asp	Leu	Lys	Tyr	Phe	Asn	Glu	Pro
	370					375					380				
Thr	Arg	Lys	Lys	Ile	Glu	Lys	Ile	Arg	Pro	Leu	Ile	Ile	Asp	Gly	Thr
385					390					395					400
Ala	Ser	Leu	Ser	Pro	Gly	Met	Met	Met	Gly	Met	Phe	Asn	Met	Leu	Ser
				405					410					415	
Thr	Val	Leu	Gly	Val	Ser	Ile	Leu	Asn	Leu	Gly	Gln	Lys	Arg	Tyr	Thr
			420					425					430		
Lys	Thr	Thr	Tyr	Trp	Trp	Asp	Gly	Leu	Gln	Ser	Ser	Asp	Asp	Phe	Ala
		435					440					445			
Leu	Ile	Val	Asn	Ala	Pro	Asn	His	Glu	Gly	Ile	Gln	Ala	Gly	Val	Asp
	450					455					460				
Arg	Phe	Tyr	Arg	Thr	Cys	Lys	Leu	Val	Gly	Ile	Asn	Met	Ser	Lys	Lys
465					470					475					480
Lys	Ser	Tyr	Ile	Asn	Arg	Thr	Gly	Thr	Phe	Glu	Phe	Thr	Ser	Phe	Phe
				485					490					495	
Tyr	Arg	Tyr	Gly	Phe	Val	Ala	Asn	Phe	Ser	Met	Glu	Leu	Pro	Ser	Phe
			500					505					510		
Gly	Val	Ser	Gly	Ile	Asn	Glu	Ser	Ala	Asp	Met	Ser	Ile	Gly	Val	Thr
		515					520					525			
Val	Ile	Lys	Asn	Asn	Met	Ile									

Gln Met Ala Leu Gln Leu Phe Ile Lys Asp Tyr Arg Tyr Thr Tyr Arg
 545 550 555 560
 Cys His Arg Gly Asp Thr Gln Ile Gln Thr Arg Arg Ser Phe Glu Ile
 565 570 575
 Lys Lys Leu Trp Glu Gln Thr His Ser Lys Ala Gly Leu Leu Val Ser
 580 585 590
 Asp Gly Gly Pro Asn Leu Tyr Asn Ile Arg Asn Leu His Ile Pro Glu
 595 600 605
 Val Cys Leu Lys Trp Glu Leu Met Asp Glu Asp Tyr Gln Gly Arg Leu
 610 615 620
 Cys Asn Pro Leu Asn Pro Phe Val Asn His Lys Asp Ile Glu Ser Val
 625 630 635 640
 Asn Asn Ala Val Ile Met Pro Ala His Gly Pro Ala Lys Asn Met Glu
 645 650 655
 Tyr Asp Ala Val Ala Thr Thr His Ser Trp Ile Pro Lys Arg Asn Arg
 660 665 670
 Ser Ile Leu Asn Thr Ser Gln Arg Gly Ile Leu Glu Asp Glu Gln Met
 675 680 685
 Tyr Gln Lys Cys Cys Asn Leu Phe Glu Lys Phe Phe Pro Ser Ser Ser
 690 695 700
 Tyr Arg Arg Pro Val Gly Ile Ser Ser Met Val Glu Ala Met Val Ser
 705 710 715 720
 Arg Ala Arg Ile Asp Ala Arg Ile Asp Phe Glu Ser Gly Arg Ile Lys
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 acaaagtgtc gcccggagta ctggtcgacc tccgaagttg ggggggagcg aaagcaggca 180
 aaccatttga atg gat gtc aat ccg act tta ctt ttc tta aaa gtg cca 229
 Met Asp Val Asn Pro Thr Leu Leu Phe Leu Lys Val Pro
 1 5 10

gca caa aat gct ata agc aca act ttc cct tat act gga gac cct cct Ala Gln Asn Ala Ile Ser Thr Thr Phe Pro Tyr Thr Gly Asp Pro Pro	277
15 20 25	
tac agc cat ggg aca gga aca gga tac acc atg gat act gtc aac agg Tyr Ser His Gly Thr Gly Thr Gly Tyr Thr Met Asp Thr Val Asn Arg	325
30 35 40 45	
aca cat cag tac tca gaa agg gga aga tgg aca aca aac acc gaa act Thr His Gln Tyr Ser Glu Arg Gly Arg Trp Thr Thr Asn Thr Glu Thr	373
50 55 60	
gga gca ccg caa ctc aac ccg att gat ggg cca ctg cca gaa gac aat Gly Ala Pro Gln Leu Asn Pro Ile Asp Gly Pro Leu Pro Glu Asp Asn	421
65 70 75	
gaa cca agt ggt tat gcc caa aca gat tgt gta ttg gaa gca atg gcc Glu Pro Ser Gly Tyr Ala Gln Thr Asp Cys Val Leu Glu Ala Met Ala	469
80 85 90	
ttc ctt gag gaa tcc cat cct ggt atc ttt gag acc tcg tgt ctt gaa Phe Leu Glu Glu Ser His Pro Gly Ile Phe Glu Thr Ser Cys Leu Glu	517
95 100 105	
acc atg gag gtt gtt cag caa aca cga gtg gac aag ctg aca caa ggc Thr Met Glu Val Val Gln Gln Thr Arg Val Asp Lys Leu Thr Gln Gly	565
110 115 120 125	
cga cag acc tat gac tgg act cta aat agg aac cag cct gct gca aca Arg Gln Thr Tyr Asp Trp Thr Leu Asn Arg Asn Gln Pro Ala Ala Thr	613
130 135 140	
gca ttg gcc aac aca ata gaa gtg ttc aga tca aat ggc ctc acg gcc Ala Leu Ala Asn Thr Ile Glu Val Phe Arg Ser Asn Gly Leu Thr Ala	661
145 150 155	
aat gaa tct gga agg ctc ata gac ttc ctt aag gat gta atg gag tca Asn Glu Ser Gly Arg Leu Ile Asp Phe Leu Lys Asp Val Met Glu Ser	709
160 165 170	
atg aac aaa gaa gaa atg gag atc aca act cat ttt cag aga aag aga Met Asn Lys Glu Glu Met Glu Ile Thr Thr His Phe Gln Arg Lys Arg	757
175 180 185	
cga gtg aga gac aat atg act aag aaa atg gtg aca cag aga aca ata Arg Val Arg Asp Asn Met Thr Lys Lys Met Val Thr Gln Arg Thr Ile	805
190 195 200 205	
ggt aaa agg aag cag aga ttg aac aaa agg agt tat cta att agg gca Gly Lys Arg Lys Gln Arg Leu Asn Lys Arg Ser Tyr Leu Ile Arg Ala	853
210 215 220	
tta acc ctg aac aca atg acc aaa gat gct gag aga ggg aag cta aaa Leu Thr Leu Asn Thr Met Thr Lys Asp Ala Glu Arg Gly Lys Leu Lys	901
225 230 235	
cgg aga gca att gca acc cca ggg atg caa ata agg ggg ttt gta tac Arg Arg Ala Ile Ala Thr Pro Gly Met Gln Ile Arg Gly Phe Val Tyr	949
240 245 250	
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255 260 265	
gga ttg cca gtt gga ggc aat gag aag aaa gca aag ttg gca aat gtt Gly Leu Pro Val Gly Gly Asn Glu Lys Lys Ala Lys Leu Ala Asn Val	1045
270 275 280 285	

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290 295 300	
atc act gga gat aac acc aaa tgg aac gaa aat cag aac cct cgg atg	1141
Ile Thr Gly Asp Asn Thr Lys Trp Asn Glu Asn Gln Asn Pro Arg Met	
305 310 315	
ttt ttg gcc atg atc aca tat ata acc aga aat cag ccc gaa tgg ttc	1189
Phe Leu Ala Met Ile Thr Tyr Ile Thr Arg Asn Gln Pro Glu Trp Phe	
320 325 330	
aga aat gtt cta agt att gct cca ata atg ttc tca aac aaa atg gcg	1237
Arg Asn Val Leu Ser Ile Ala Pro Ile Met Phe Ser Asn Lys Met Ala	
335 340 345	
aga ctg gga aag ggg tac atg ttt gag agc aag agt atg aaa att aga	1285
Arg Leu Gly Lys Gly Tyr Met Phe Glu Ser Lys Ser Met Lys Ile Arg	
350 355 360 365	
act caa ata cct gca gaa atg cta gca agt att gat cta aaa tat ttc	1333
Thr Gln Ile Pro Ala Glu Met Leu Ala Ser Ile Asp Leu Lys Tyr Phe	
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Asn Glu Pro Thr Arg Lys Lys Ile Glu Lys Ile Arg Pro Leu Leu Ile	
385 390 395	
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Asp Gly Thr Ala Ser Leu Ser Pro Gly Met Met Met Gly Met Phe Asn	
400 405 410	
atg tta agt act gta tta ggc gtc tcc atc ctg aat ctt gga caa aag	1477
Met Leu Ser Thr Val Leu Gly Val Ser Ile Leu Asn Leu Gly Gln Lys	
415 420 425	
aga cac acc aag act act tac tgg tgg gat ggt ctt caa tct tct gat	1525
Arg His Thr Lys Thr Thr Tyr Trp Trp Asp Gly Leu Gln Ser Ser Asp	
430 435 440 445	
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Asp Phe Ala Leu Ile Val Asn Ala Pro Asn His Glu Gly Ile Gln Ala	
450 455 460	
gga gtc aac agg ttt tat cga acc tgt aag cta ctt gga att aat atg	1621
Gly Val Asn Arg Phe Tyr Arg Thr Cys Lys Leu Leu Gly Ile Asn Met	
465 470 475	
agc aag aaa aag tct tac ata aac aga aca ggt aca ttt gaa ttc aca	1669
Ser Lys Lys Lys Ser Tyr Ile Asn Arg Thr Gly Thr Phe Glu Phe Thr	
480 485 490	
agc ttt ttc tat cgt tat ggg ttt gtt gcc aat ttc agc atg gag ctt	1717
Ser Phe Phe Tyr Arg Tyr Gly Phe Val Ala Asn Phe Ser Met Glu Leu	
495 500 505	
ccc agc ttt ggg gtg tct ggg atc aac gag tct gcg gac atg agt att	1765
Pro Ser Phe Gly Val Ser Gly Ile Asn Glu Ser Ala Asp Met Ser Ile	
510 515 520 525	
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Gly Val Thr Val Ile Lys Asn Asn Met Ile Asn Asn Asp Leu Gly Pro	
530 535 540	
gca acc gct caa atg gcc ctt cag ctg ttc atc aaa gat tac agg tac	1861

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Ala Thr Ala Gln Met Ala Leu Gln Leu Phe Ile Lys Asp Tyr Arg Tyr
545 550 555

acg tac cgg tgc cat aga ggt gac aca caa ata caa acc cga aga tca 1909
Thr Tyr Arg Cys His Arg Gly Asp Thr Gln Ile Gln Thr Arg Arg Ser
560 565 570

ttt gaa ata aag aaa ctg tgg gag caa acc cat tcc aaa gct gga ctg 1957
Phe Glu Ile Lys Lys Leu Trp Glu Gln Thr His Ser Lys Ala Gly Leu
575 580 585

ctg gtc tcc gac gga ggc cca aat tta tac aac att aga aat ctc cac 2005
Leu Val Ser Asp Gly Gly Pro Asn Leu Tyr Asn Ile Arg Asn Leu His
590 595 600 605

att cct gaa gtc tgc ttg aaa tgg gaa tta atg gat gag gat tac cag 2053
Ile Pro Glu Val Cys Leu Lys Trp Glu Leu Met Asp Glu Asp Tyr Gln
610 615 620

ggg cgt tta tgc aac cca ctg aac cca ttt gtc aac cat aaa gac att 2101
Gly Arg Leu Cys Asn Pro Leu Asn Pro Phe Val Asn His Lys Asp Ile
625 630 635

gaa tca gtg aac aat gca gtg ata atg cca gca cat ggt cca gcc aaa 2149
Glu Ser Val Asn Asn Ala Val Ile Met Pro Ala His Gly Pro Ala Lys
640 645 650

aac atg gag tat gat gct gtt gca aca aca cac tcc tgg atc ccc aaa 2197
Asn Met Glu Tyr Asp Ala Val Ala Thr Thr His Ser Trp Ile Pro Lys
655 660 665

aga aat cga tcc atc ttg aat aca agc caa aga gga ata ctt gaa gat 2245
Arg Asn Arg Ser Ile Leu Asn Thr Ser Gln Arg Gly Ile Leu Glu Asp
670 675 680 685

gaa caa atg tac caa aag tgc tgc aac tta ttt gaa aaa ttc ttc ccc 2293
Glu Gln Met Tyr Gln Lys Cys Cys Asn Leu Phe Glu Lys Phe Phe Pro
690 695 700

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705 710 715

atg gtt tcc aga gcc cga att gat gca cga att gat ttc gaa tct gga 2389
Met Val Ser Arg Ala Arg Ile Asp Ala Arg Ile Asp Phe Glu Ser Gly
720 725 730

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Arg Ile Lys Lys Glu Glu Phe Thr Glu Ile Met Lys Ile Cys Ser Thr
735 740 745

att gaa gag ctc aga cgg caa aaa tagtgaattt agcttgtcct tcatgaaaa 2491
Ile Glu Glu Leu Arg Arg Gln Lys
750 755

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 Tyr Ser Glu Arg Gly Arg Trp Thr Thr Asn Thr Glu Thr Gly Ala Pro
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 Gln Leu Asn Pro Ile Asp Gly Pro Leu Pro Glu Asp Asn Glu Pro Ser
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 Glu Ser His Pro Gly Ile Phe Glu Thr Ser Cys Leu Glu Thr Met Glu
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 Val Val Gln Gln Thr Arg Val Asp Lys Leu Thr Gln Gly Arg Gln Thr
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 Glu Glu Met Glu Ile Thr Thr His Phe Gln Arg Lys Arg Arg Val Arg
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 Asp Asn Met Thr Lys Lys Met Val Thr Gln Arg Thr Ile Gly Lys Arg
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 Lys Gln Arg Leu Asn Lys Arg Ser Tyr Leu Ile Arg Ala Leu Thr Leu
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Thr Leu Ala Arg Ser Ile Cys Glu Lys Leu Glu Gln Ser Gly Leu Pro
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 Leu Ser Ile Ala Pro Ile Met Phe Ser Asn Lys Met Ala Arg Leu Gly
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 Lys Lys Leu Trp Glu Gln Thr His Ser Lys Ala Gly Leu Leu Val Ser
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Cys Asn Pro Leu Asn Pro Phe Val Asn His Lys Asp Ile Glu Ser Val
625 630 635 640

Asn Asn Ala Val Ile Met Pro Ala His Gly Pro Ala Lys Asn Met Glu
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Tyr Asp Ala Val Ala Thr Thr His Ser Trp Ile Pro Lys Arg Asn Arg
660 665 670

Ser Ile Leu Asn Thr Ser Gln Arg Gly Ile Leu Glu Asp Glu Gln Met
675 680 685

Tyr Gln Lys Cys Cys Asn Leu Phe Glu Lys Phe Phe Pro Ser Ser Ser
690 695 700

Tyr Arg Arg Pro Val Gly Ile Ser Ser Met Val Glu Ala Met Val Ser
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Arg Ala Arg Ile Asp Ala Arg Ile Asp Phe Glu Ser Gly Arg Ile Lys
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Ala Gln Asn Ala Ile Ser Thr Thr Phe Pro Tyr Thr Gly Asp Pro Pro
15 20 25

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Tyr Ser His Gly Thr Gly Thr Gly Tyr Thr Met Asp Thr Val Asn Arg
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Thr His Gln Tyr Ser Glu Arg Gly Arg Trp Thr Thr Asn Thr Glu Thr
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 Glu Pro Ser Gly Tyr Ala Gln Thr Asp Cys Val Leu Glu Ala Met Ala
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 Phe Leu Glu Glu Ser His Pro Gly Ile Phe Glu Thr Ser Cys Leu Glu
 95 100 105

acg atg gag gtt gtt cag caa aca cga gtg gac aag ctg aca caa ggc 565
 Thr Met Glu Val Val Gln Gln Thr Arg Val Asp Lys Leu Thr Gln Gly
 110 115 120 125

cga cag acc tat gac tgg act cta aat agg aac cag cct gct gca aca 613
 Arg Gln Thr Tyr Asp Trp Thr Leu Asn Arg Asn Gln Pro Ala Ala Thr
 130 135 140

gca ttg gcc aac aca ata gaa gtg ttc aga tca aat ggc ctc acg gcc 661
 Ala Leu Ala Asn Thr Ile Glu Val Phe Arg Ser Asn Gly Leu Thr Ala
 145 150 155

aat gaa tct gga agg ctc ata gac ttc ctt aag gat gta atg gag tca 709
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 160 165 170

atg aac aaa gaa gaa atg gag atc aca act cat ttt cag aga aag aga 757
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cga gtg aga gac aat atg act aag aaa atg gtg aca cag aga aca ata 805
 Arg Val Arg Asp Asn Met Thr Lys Lys Met Val Thr Gln Arg Thr Ile
 190 195 200 205

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 210 215 220

tta acc ctg aac aca atg acc aaa gat gct gag aga ggg aag cta aaa 901
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 225 230 235

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 Phe Val Glu Thr Leu Ala Arg Ser Ile Cys Glu Lys Leu Glu Gln Ser
 255 260 265

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 Gly Leu Pro Val Gly Gly Asn Glu Lys Lys Ala Lys Leu Ala Asn Val
 270 275 280 285

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 415 420 425

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Arg Ala Arg Ile Asp Ala Arg Ile Asp Phe Glu Ser Gly Arg Ile Lys
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aaccatttga atg gat gtc aat ccg act tta ctt ttc tta aaa gtg cca 229
Met Asp Val Asn Pro Thr Leu Leu Phe Leu Lys Val Pro
1 5 10

gca caa aat gct ata agc aca act ttc cct tat act gga gac cct cct 277
Ala Gln Asn Ala Ile Ser Thr Thr Phe Pro Tyr Thr Gly Asp Pro Pro
15 20 25

tac agc cat ggg aca gga aca gga tac acc atg gat act gtc aac agg 325
Tyr Ser His Gly Thr Gly Thr Gly Tyr Thr Met Asp Thr Val Asn Arg
30 35 40 45

aca cat cag tac tca gaa agg gga aga tgg aca aca aac acc gaa act 373
Thr His Gln Tyr Ser Glu Arg Gly Arg Trp Thr Thr Asn Thr Glu Thr
50 55 60

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Gly Ala Pro Gln Leu Asn Pro Ile Asp Gly Pro Leu Pro Glu Asp Asn
65 70 75

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Glu Pro Ser Gly Tyr Ala Gln Thr Asp Cys Val Leu Glu Ala Met Ala
80 85 90

ttc ctt gag gaa tcc cat cct ggt atc ttt gag acc tcg tgt ctt gaa 517
Phe Leu Glu Glu Ser His Pro Gly Ile Phe Glu Thr Ser Cys Leu Glu
95 100 105

acg atg gag gtt gtt cag caa aca cga gtg gac aag ctg aca caa ggc 565

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Thr Met Glu Val Val Gln Gln Thr Arg Val Asp Lys Leu Thr Gln Gly
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 Arg Gln Thr Tyr Asp Trp Thr Leu Asn Arg Asn Gln Pro Ala Ala Thr
 130 135 140

gca ttg gcc aac aca ata gaa gtg ttc aga tca aat ggc ctc acg gcc 661
 Ala Leu Ala Asn Thr Ile Glu Val Phe Arg Ser Asn Gly Leu Thr Ala
 145 150 155

aat gaa tct gga agg ctc ata gac ttc ctt aag gat gta atg gag tca 709
 Asn Glu Ser Gly Arg Leu Ile Asp Phe Leu Lys Asp Val Met Glu Ser
 160 165 170

atg aac aaa gaa gaa atg gag atc aca act cat ttt cag aga aag aga 757
 Met Asn Lys Glu Glu Met Glu Ile Thr Thr His Phe Gln Arg Lys Arg
 175 180 185

cga gtg aga gac aat atg act aag aaa atg gtg aca cag aga aca ata 805
 Arg Val Arg Asp Asn Met Thr Lys Lys Met Val Thr Gln Arg Thr Ile
 190 195 200 205

ggt aaa agg aag cag aga ttg aac aaa agg agt tat cta att agg gca 853
 Gly Lys Arg Lys Gln Arg Leu Asn Lys Arg Ser Tyr Leu Ile Arg Ala
 210 215 220

tta acc ctg aac aca atg acc aaa gat gct gag aga ggg aag cta aaa 901
 Leu Thr Leu Asn Thr Met Thr Lys Asp Ala Glu Arg Gly Lys Leu Lys
 225 230 235

cgg aga gca att gca acc cca ggg atg caa ata agg ggg ttt gta tac 949
 Arg Arg Ala Ile Ala Thr Pro Gly Met Gln Ile Arg Gly Phe Val Tyr
 240 245 250

ttt gtt gag aca cta gca agg agt ata tgt gag aaa ctt gaa caa tca 997
 Phe Val Glu Thr Leu Ala Arg Ser Ile Cys Glu Lys Leu Glu Gln Ser
 255 260 265

gga ttg cca gtt gga ggc aat gag aag aaa gca aag ttg gca aat gtt 1045
 Gly Leu Pro Val Gly Gly Asn Glu Lys Lys Ala Lys Leu Ala Asn Val
 270 275 280 285

gta agg aag atg atg acc aat tct cag gac act gaa att tct ttc acc 1093
 Val Arg Lys Met Met Thr Asn Ser Gln Asp Thr Glu Ile Ser Phe Thr
 290 295 300

atc act gga gat aac acc aaa tgg aac gaa aat cag aac cct cgg atg 1141
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 305 310 315

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 Phe Leu Ala Met Ile Thr Tyr Ile Thr Arg Asn Gln Pro Glu Trp Phe
 320 325 330

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 Arg Asn Val Leu Ser Ile Ala Pro Ile Met Phe Ser Asn Lys Met Ala
 335 340 345

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 Arg Leu Gly Lys Gly Tyr Met Phe Glu Ser Lys Ser Met Lys Ile Arg
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 Gln Leu Asn Pro Ile Asp Gly Pro Leu Pro Glu Asp Asn Glu Pro Ser
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 Met Ile Thr Tyr Ile Thr Arg Asn Gln Pro Glu Trp Phe Arg Asn Val
 325 330 335
 Leu Ser Ile Ala Pro Ile Met Phe Ser Asn Lys Met Ala Arg Leu Gly
 340 345 350
 Lys Gly Tyr Met Phe Glu Ser Lys Ser Met Lys Ile Arg Thr Gln Ile
 355 360 365
 Pro Ala Glu Met Leu Ala Ser Ile Asp Leu Lys Tyr Phe Asn Glu Pro
 370 375 380

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Thr Arg Lys Lys Ile Glu Lys Ile Arg Pro Leu Leu Ile Asp Gly Thr
 385 390 395 400
 Ala Ser Leu Ser Pro Gly Met Met Met Gly Met Phe Asn Met Leu Ser
 405 410 415
 Thr Val Leu Gly Val Ser Ile Leu Asn Leu Gly Gln Lys Arg His Thr
 420 425 430
 Lys Thr Thr Tyr Trp Trp Asp Gly Leu Gln Ser Ser Asp Asp Phe Ala
 435 440 445
 Leu Ile Val Asn Ala Pro Asn His Glu Gly Ile Gln Ala Gly Val Asn
 450 455 460
 Arg Phe Tyr Arg Thr Cys Lys Leu Leu Gly Ile Asn Met Ser Lys Lys
 465 470 475 480
 Lys Ser Tyr Ile Asn Arg Thr Gly Thr Phe Glu Phe Thr Ser Phe Phe
 485 490 495
 Tyr Arg Tyr Gly Phe Val Ala Asn Phe Ser Met Glu Leu Pro Ser Phe
 500 505 510
 Gly Val Ser Gly Ile Asn Glu Ser Ala Asp Met Ser Ile Gly Val Thr
 515 520 525
 Val Ile Lys Asn Asn Met Ile Asn Asn Asp Leu Gly Pro Ala Thr Ala
 530 535 540
 Gln Met Ala Leu Gln Leu Phe Ile Lys Asp Tyr Arg Tyr Thr Tyr Arg
 545 550 555 560
 Cys His Arg Gly Asp Thr Gln Ile Gln Thr Arg Arg Ser Phe Glu Ile
 565 570 575
 Lys Lys Leu Trp Glu Gln Thr His Ser Lys Ala Gly Leu Leu Val Ser
 580 585 590
 Asp Gly Gly Pro Asn Leu Tyr Asn Ile Arg Asn Leu His Ile Pro Glu
 595 600 605
 Val Cys Leu Lys Trp Glu Leu Met Asp Glu Asp Tyr Gln Gly Arg Leu
 610 615 620
 Cys Asn Pro Met Asn Pro Phe Val Ser His Lys Glu Ile Glu Ser Val
 625 630 635 640
 Asn Asn Ala Ala Val Met Pro Ala His Gly Pro Ala Lys Ser Met Glu
 645 650 655
 Tyr Asp Ala Val Ala Thr Thr His Ser Trp Ile Pro Lys Arg Asn Arg
 660 665 670
 Ser Ile Leu Asn Thr Ser Gln Arg Gly Ile Leu Glu Asp Glu Gln Met
 675 680 685
 Tyr Gln Lys Cys Cys Asn Leu Phe Glu Lys Phe Phe Pro Ser Ser Ser
 690 695 700
 Tyr Arg Arg Pro Val Gly Ile Ser Ser Met Val Glu Ala Met Val Ser
 705 710 715 720
 Arg Ala Arg Ile Asp Ala Arg Ile Asp Phe Glu Ser Gly Arg Ile Lys
 725 730 735

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Lys Glu Glu Phe Ala Glu Ile Met Lys Ile Cys Ser Thr Ile Glu Glu
740 745 750

Leu Arg Arg Gln Lys
755

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